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DB=USPT; PLUR=YES; OP=AND

☐	L1	vc167 or vc-167	13
☐	L2	L1 and campylobac$	13
☐	L3	L1 same campylobac$	12
☐	L4	(flaa or fla-a or flagel$).ti,ab,clm.	123
☐	L5	L4 and campylobac$	19

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	**FLB2_CAMJE**
Primary accession number	**P22252**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 19, August 1991
Sequence was last modified in	Release 34, October 1996
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	**Flagellin B**
Synonyms	None
Gene name	**Name: flaB**
From	Campylobacter jejuni [TaxID: 197]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=81116;
MEDLINE=91009243;PubMed=2211662 [NCBI, ExPASy, EBI, Israel, Japan]
Nuijten P.J., van Asten F.J., Gaastra W., van der Zeijst B.A.;
"Structural and functional analysis of two Campylobacter jejuni flagellin genes.";
J. Biol. Chem. 265:17798-17804(1990).

Comments

- *FUNCTION*: Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella.
- *SUBUNIT*: Heteropolymer of flaA and flaB.
- *SIMILARITY*: Belongs to the bacterial flagellin family.

Copyright

Cross-references

EMBL	J05635; AAA23025.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	B39228; B39228.
InterPro	IPR001029; Flagellin_C. IPR010810; Flagellin_IN. IPR001492; Flagellin_N. Graphical view of domain structure.
Pfam	PF00700; Flagellin_C; 1. PF07196; Flagellin_IN; 2. PF00669; Flagellin_N; 1. Pfam graphical view of domain structure.
PRINTS	PR00207; FLAGELLIN.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P22252.
ProtoNet	P22252.
ProtoMap	P22252.
PRESAGE	P22252.
DIP	P22252.
ModBase	P22252.
SMR	P22252; D0531AF308A7BF1D.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features
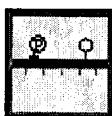
 Feature table viewer

```
Key        From To  Length   Description
INIT_MET     0   0           By similarity.
```

Sequence information

Length: **575 AA**   Molecular weight: **59728 Da**   CRC64: **D0531AF308A7BF1D** [This is a checksum on the sequence]

```
         10          20          30          40          50          60
          |           |           |           |           |           |
GFRINTNIGA LNAHANSVVN SNELDKSLSR LSSGLRINSA ADDASGMAIA DSLRSQAATL

         70          80          90         100         110         120
          |           |           |           |           |           |
GQAINNGNDA IGILQTADKA MDEQLKILDT IKTKATQAAQ DGQSLKTRTM LQADINRLME

        130         140         150         160         170         180
          |           |           |           |           |           |
ELDNIANTTS FNGKQLLSGN FTNQEFQIGA SSNQTIKATI GATQSSKIGV TRFETGAQSF

        190         200         210         220         230         240
```

```
           |          |          |          |          |          |
  TSGVVGLTIK NYNGIEDFKF DNVVISTSVG TGLGALAEEI NKSADKTGVR ATYDVKTTGV

         250        260        270        280        290        300
           |          |          |          |          |          |
  YAIKEGTTSQ DFAINGVVIG QINYKDGDNN GQLVSAINAV KDTTGVQASK DENGKLVLTS

         310        320        330        340        350        360
           |          |          |          |          |          |
  ADGRGIKITG DIGVGSGILA NQKENYGRLS LVKNDGRDIN ISGTNLSAIG MGTTDMISQS

         370        380        390        400        410        420
           |          |          |          |          |          |
  SVSLRESKGQ ISATNADAMG FNSYKGGGKF VFTQNVSSIS AFMSAQGSGF SRGSGFSVGS

         430        440        450        460        470        480
           |          |          |          |          |          |
  GKNLSVGLSQ GIQIISSAAS MSNTYVVSAG SGFSSGSGNS QFAALKTTAA NTTDETAGVT

         490        500        510        520        530        540
           |          |          |          |          |          |
  TLKGAMAVMD IAETAITNLD QIRADIGSVQ NQLQVTINNI TVTQVNVKAA ESTIRDVDFA

         550        560        570
           |          |          |
  SESANFSKYN ILAQSGSYAM SQRNAVQQNV LKLLQ
```

P22252 in FASTA
format

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ScanProsite, MotifScan

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Hit List

Search Results - Record(s) 1 through 12 of 12 returned.

☐ 1. Document ID: US 6413523 B1

L3: Entry 1 of 12   File: USPT   Jul 2, 2002

DOCUMENT-IDENTIFIER: US 6413523 B1
TITLE: Pharmaceutical composition of escherichia coli heat-labile enterotoxin
adjuvant and methods of use

Detailed Description Paragraph Table (1):
TABLE 6 Adjuvant Admministered With Campylobacter Antigen Confers Protection Against
Against Subsequent Challenge Rabbits Rabbits Colonization Number immunized with
challenged with.sup.1 (days + S.D.) resistant.sup.2 -- VC167 8.1 + 1.2 0/6 3 (OA)
VC167 8.0 + 1.0 0/7 3 (SON).sup.3 VC167 7.0 + 1.0 1/8 3 (SON + OA) VC167 2.7 + 2.4
9/11 3 (SON) + 1 (OA) VC167 8.0 + 0.8 0/4 -- 81116 7.6 + 0.6 1/3 3 (SON + OA) 81116
6.0 + 1.0 1/4 .sup.1 VC167 is a Lior 8 strain of C. coli and 81116 is a Lior 6
strain of C. jejuni .sup.2 Number of animals negative for Campylobacter 5 days
after RITARD challenge/total number in group .sup.3 Sonicates (SON) used for
immunization were prepared from VC167

Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw De

☐ 2. Document ID: US 6221582 B1

L3: Entry 2 of 12   File: USPT   Apr 24, 2001

DOCUMENT-IDENTIFIER: US 6221582 B1
TITLE: Polynucleic acid sequences for use in the detection and differentiation of
prokaryotic organisms

Detailed Description Text (8):
At present a few PCR assays for the detection of Campylobacter in food,
environmental and clinical samples have been described. Oyofo et al. (1992)
developed a PCR based on the 5' end of the flaA gene of C. coli VC167. Wegmuller et
al. (1993) designed a PCR assay based on the intergenic sequence between the
flagellin genes flaA and flaB. Stonnet & Guesdon (1993) developed a PCR test
specific for C. jejuni, based on a DNA fragment isolated from a C. jejuni CIP70.2
cosmid library. Van Camp et al. (1993) used the 16S rRNA gene and described a PCR
assay that could not discriminate between the different thermophilic Campylobacter
species. Eyers et al. (1993), however, developed a Campylobacter species-specific
PCR assay based on the region located between helices 43 and 69 of the 23S rRNA.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw De |

☐ 3.   Document ID: US 6083683 A

L3: Entry 3 of 12   File: USPT   Jul 4, 2000

DOCUMENT-IDENTIFIER: US 6083683 A
TITLE: Methods for detecting shigella bacteria or antibodies to shigella bacteria
with an immunoassay

Detailed Description Text (164):
It should be further noted that strains of Lior serotype 8 are of a different
species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly
agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a
vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect
against heterologous serotypes within the same species, but also other
Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior
serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated
serotypes world-wide. They all demonstrated detectable cross-reactivity in this
assay.

Detailed Description Paragraph Table (17):
TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134
1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++
6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - -
- 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
- ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -
_____ .sup.a The anti81-176 mucus were obtained
from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The
nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination
responses range from negative (-), to very weak (.+-.), to very strong (++++)

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw De |

☐ 4.   Document ID: US 6077678 A

L3: Entry 4 of 12   File: USPT   Jun 20, 2000

DOCUMENT-IDENTIFIER: US 6077678 A
TITLE: Methods for detecting Campylobacter bacteria or antibodies to Campylobacter
bacteria with an immunoassay

Detailed Description Text (135):
It should be further noted that strains of Lior serotype 8 are of a different

species, <u>Campylobacter</u> coli. One of the 2 strains (<u>VC167</u>) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other <u>Campylobacter</u> species (e.g., <u>Campylobacter</u> coli). Also worth noting is that Lior serotypes 1, 2; 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

<u>Detailed Description Paragraph Table</u> (16):
TABLE 16 _____ Agglutination Response of 20 <u>Campylobacter</u> Serotypes Grown Conventionally (BHI-YE) or According to the Methods of of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134 1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++ 6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ <u>VC-167</u> 8 - - + +++ VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - - - 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - - + +++ 1982 29 - - - - 910 32 - ++ - ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - - _____ .sup.a The anti81-176 mucus were obtained from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.+-.), to very strong (++++)

CLAIMS:

4. The method according to claim 3, wherein said <u>Campylobacter</u> bacterium is a <u>Campylobacter</u> jejuni strain selected from the group consisting of 134, 195, 170, 81-81-176, 6, 81-116, 35, 52, <u>VC-167,</u> 88, 244, 544, 699, 1180, 910, and HC.

11. The method according to claim 10 wherein said <u>Campylobacter</u> bacterium is a <u>Campylobacter</u> jejuni strain selected from the group consisting of 134, 195, 170, 81-81-176, 6, 81-116, 35, 52, <u>VC-167,</u> 88, 244, 544, 699, 1180, 910, and HC.

18. The diagnostic immunoassay kit according to claim 17, wherein said <u>Campylobacter</u> bacterium is a <u>Campylobacter</u> jejuni strain selected from the group consisting of 134, 195, 170, 81-176, 6, 81-116, 35, 52, <u>VC-167,</u> 88, 244, 544, 699, 1180,910, and HC.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw. D |

□ 5.   Document ID: US 6051416 A

L3: Entry 5 of 12   File: USPT   Apr 18, 2000

DOCUMENT-IDENTIFIER: US 6051416 A
TITLE: Methods for producing enhanced antigenic Helicobacter sp.

<u>Detailed Description Text</u> (161):
It should be further noted that strains of Lior serotype 8 are of a different species, <u>Campylobacter</u> coli. One of the 2 strains (<u>VC167</u>) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a

vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):
TABLE 16 _____ Agglutination Response of 20 Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134 1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++ 6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - - 52 8 - + + ++ VC-167 8 - - + +++ VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - - - 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++ - ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - - _____ .sup.a The anti81-176 mucus were obtained from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.+-.), to very strong (++++)

☐ 6.   Document ID: US 5976525 A

L3: Entry 6 of 12   File: USPT   Nov 2, 1999

DOCUMENT-IDENTIFIER: US 5976525 A
TITLE: Method for producing enhanced antigenic enteric bacteria

Detailed Description Text (128):
It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):
TABLE 16 _____ Agglutination Response of 20 Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134 1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++ 6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++ VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - - - 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++ - ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - - _____ .sup.a The anti81-176 mucus were obtained

from rabbits infected with live C. jejuni 81-176 grown conventionally .sup.b The
nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination
responses range from negative (-), to very weak (.+-.), to very strong (+++)

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

□ 7. Document ID: US 5897475 A

L3: Entry 7 of 12   File: USPT   Apr 27, 1999

DOCUMENT-IDENTIFIER: US 5897475 A
TITLE: Vaccines comprising enhanced antigenic helicobacter spp.

Detailed Description Text (166):
It should be further noted that strains of Lior serotype 8 are of a different
species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly
agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a
vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect
against heterologous serotypes within the same species, but also other
Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior
serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated
serotypes world-wide. They all demonstrated detectable cross-reactivity in this
assay.

Detailed Description Paragraph Table (16):
TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134
1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++
6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - -
- 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
- ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -
_____ .sup.a The anti81-176 mucus were obtained
from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The
nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination
responses range from negative (-), to very weak (.+-.), to very strong (+++)

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

□ 8. Document ID: US 5869066 A

L3: Entry 8 of 12   File: USPT   Feb 9, 1999

DOCUMENT-IDENTIFIER: US 5869066 A
TITLE: Vaccine containing a campylobacter bacterium having an enhanced antigenic
property

Detailed Description Text (166):
It should be further noted that strains of Lior serotype 8 are of a different
species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly
agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a
vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect
against heterologous serotypes within the same species, but also other
Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior
serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated
serotypes world-wide. They all demonstrated detectable cross-reactivity in this
assay.

Detailed Description Paragraph Table (16):
TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134
1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++
6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - -
- 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
- ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -
_____ .sup.a The anti81-176 mucus were obtained
from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The
nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination
responses range from negative (-), to very weak (.+-.), to very strong (++++)

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 Full | Title | Citation | Front | Review | Classification | Date | Reference |        |        | Claims | KWIC | Draw De
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□ 9. Document ID: US 5858352 A
L3: Entry 9 of 12   File: USPT   Jan 12, 1999

DOCUMENT-IDENTIFIER: US 5858352 A
TITLE: Vaccine containing a Shigella bacterium having an enhanced antigenic
property

Detailed Description Text (167):
It should be further noted that strains of Lior serotype 8 are of a different
species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly
agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a
vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect
against heterologous serotypes within the same species, but also other
Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior
serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated
serotypes world-wide. They all demonstrated detectable cross-reactivity in this
assay.

Detailed Description Paragraph Table (16):
TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response Lior Non-immune mucus Immune Mucus Strain Serotype
BHI-YE ENHANCED BHI-YE ENHANCED _____ 134 1 - - -

++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++ 6 6 - -
++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++ VC-159 8 -
- .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - - - 544 19 -
++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++ - ++ 2074
36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -

_____ .sup.a The anti81-176 mucus were obtained
from rabbits infected with live C. jejuni 81-176 grown conventionally .sup.b The
nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination
responses range from negative (-), to very weak (.+-.), to very strong (++++)

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

☐ 10. Document ID: US 5681736 A

L3: Entry 10 of 12   File: USPT   Oct 28, 1997

DOCUMENT-IDENTIFIER: US 5681736 A
TITLE: Methods for producing enhanced antigenic shigella bacteria and vaccines
comprising same

Detailed Description Text (122):
It should be further noted that strains of Lior serotype 8 are of a different
species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly
agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a
vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect
against heterologous serotypes within the same species, but also other
Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior
serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated
serotypes world-wide. They all demonstrated detectable cross-reactivity in this
assay.

Detailed Description Paragraph Table (16):
TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134
1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++
6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - -
- 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
- ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

☐ 11. Document ID: US 5679564 A

L3: Entry 11 of 12   File: USPT   Oct 21, 1997

DOCUMENT-IDENTIFIER: US 5679564 A
TITLE: Methods for producing enhanced antigenic campylobacter bacteria and vaccines

Detailed Description Text (120):
It should be further noted that strains of Lior serotype 8 are of a different
species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly
agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a
vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect
against heterologous serotypes within the same species, but also other
Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior
serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated
serotypes world-wide. They all demonstrated detectable cross-reactivity in this
assay.

Detailed Description Paragraph Table (16):
TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134
1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - +++ ++++ 81-176 5 - - ++++ ++++
6 6 - - ++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - -
- 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
- ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -
_____ .sup.a The anti81-176 mucus were obtained
from rabbits infected with live C. jejuni 81-176 grown conventionally .sup.b The
nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination
responses range from negative (-), to very weak (.+-.), to very strong (++++)

CLAIMS:

4. The method according to claim 3, wherein said Campylobacter species is a
Campylobacter jejuni strain selected from the group consisting of 134, 195, 170, 81-
81-176, 6, 81-116, 35, 52, VC-167, 88, 244, 544, 699, 1180, 910, and HC.

10. The Campylobacter bacterium according to claim 9, wherein said Campylobacter
species is a Campylobacter jejuni strain selected from the group consisting of 134,
195, 170, 81-176, 6, 81-116, 35, 52, VC-167, 88, 244, 544, 699, 1180, 910, and HC.

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw D |

_____

☐ 12. Document ID: US 5494795 A
L3: Entry 12 of 12   File: USPT   Feb 27, 1996

DOCUMENT-IDENTIFIER: US 5494795 A
TITLE: Specific oligonucleotide primers for detection of pathogenic campylobacter
bacteria by polymerase chain reaction

Brief Summary Text (11):
These and additional objects of the invention are accomplished by application of

standard PCR methodology employing the oligonucleotide primers pg50 (5'-ATGGGATTTCGTATTAAC-3'(SEQ ID No. 1)) and pg3 (5'-GAACTTGAACCGATTTG-3'(SEQ ID No. 2))
2)) to amplify DNA from the flaA flagellin gene of Campylobacter coli strain VC167
and the digoxigenin-labeled probe pBA273 to detect the amplified DNA in fecal
specimens (extracted by the method of G. Frankel, et al., Mol. Microbiol. 3:1729-1734, 1989) of animals and humans.

Detailed Description Text (4):
Two oligonucleotides, pg50 (5'-ATGGGATTTCGTATTAAC-3'(SEQ ID No. 1)) and pg3 (5'-GAACTTGAACCGATTTG-3'(SEQ ID No 2)), have been selected from the DNA sequence of the
flaA flagellin gene (base pairs 289-2007, GenBank Accession No. M64670) of C. coli
strain VC167 (see FIG. 1); pg50 is between base pairs 289-306 and pg3 is between
base pairs 730-746 on the minus strand. These two oligonucleotides function as
specific primers for PCR amplification of C. coli and C. jejuni DNA. A probe
internal to the amplified gene region was constructed by standard methods (T.
Maniatis, et al., Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab.,
Cold Spring Harbor, N.Y., 1982) for detection of the PCR-amplified Campylobacter
DNA. The probe lies between base pairs 481-759 of the DNA in GenBank Accession No.
M64670. The results were reported by poster presentation at the American Society
for Microbiology on 30 May 1992 (Abstracts of the General Meeting, D-206, p. 130)
and in the J. Clin. Microbiol. 30:2613-2619, 1992, by the inventors, and are
described in detail below.

Detailed Description Text (12):
The oligonucleotide primers pg50 (5'-ATGGGATTTCGTATTAAC-3'(SEQ ID No. 1)) and pg3
(5'-GAACTTGAACCGATTTG-3'(SEQ ID No. 2)) derived from the well-conserved amino
terminus of the flaA flagellin gene of Campylobacter coli strain VC167 (P. Guerry,
et al., J. Bacteriol. 172:1853-1860, 1990; cf. FIG. 1) were selected following
comparison of 30 strains of C. coli and C. jejuni by DNA hybridization (S. A.
Thornton., et al., Infect. Immun. 58:2686-2698, 1990) and N-terminal amino acid
sequencing of flagella from various strains of C. coli and C. jejuni. These
oligonucleotide sequences represent well-conserved but distinctive DNA sequences in
the flaA N-termini of both C. coli and C. jejuni but are not present in DNA
sequences of other Campylobacter spp. such J. Clinical Microbiology 1992). Primer
pg50 binds to the beginning of flaA but not flaB; primer pg3 binds to the second
strand 450 base pairs downstream from the pg50-binding site on flaA as well as at
the corresponding position of flaB.

Detailed Description Text (24):
Using the digoxigenin-labeled pBA273 probe, serial dilutions of DNA extracted from
cultured VC167 bacteria were subjected to PCR amplification using the pg3-pg50
primers, and the products were electrophoresed and transferred to a nylon membrane
by Southern blotting (T. Maniatis, et al., ibid) and hybridized in 533 SSC buffer
(1.times.SSC=0.015 M sodium citrate-0.15 M sodium chloride) for 16-24 hr at
60.degree. C. with 230 ng of digoxigenin-labeled probe per 100 cm.sup.2 of
membrane. The results indicate that the PCR products generated with as little as
0.062 pg of DNA can be visualized on the agarose gel and that hybridization with
the internal probe allows detection of a little as 0.0062 pg of DNA. Based on the
genome size for Campylobacter spp. of 1,700 kilobase pairs, this corresponds to four
four or fewer bacteria.

Detailed Description Text (26):
In order to evaluate the feasibility of direct PCR detection of campylobacters in
fecal material, rectal swabs were taken from 15 rabbits which were fed VC167 2 days
prior to sampling, and from 15 control rabbits which had been fed sterile culture
broth. Following transport to the laboratory in Cary Blair medium, aliquots of
fecal material from each rabbit were re-suspended in phosphate buffered saline as
described above. An aliquot from each sample was plated directly onto campylobacter
blood agar and the plates were incubated microaerobically for 48 h. Another aliquot
was processed for PCR using the extraction method of Frankel et al. (ibid), the

products were dot blotted, and hybridized to the non-radioactively labelled internal internal probe from pBA273. The PCR assay detected C. coli in all 15 infected rabbits, although only 12/15 rabbits were positive by plating. No campylobacters were detected in the uninfected control rabbits by either PCR or plating.

Detailed Description Paragraph Table (2):

SEQUENCE LISTING (1) GENERAL INFORMATION: (iii) NUMBER OF SEQUENCES: 2 (2) INFORMATION FOR SEQ ID NO:1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Campylobacter coli (B) STRAIN: VC167 (x) PUBLICATION INFORMATION: (A) AUTHORS: Oyofo, Buhari A Thornton, Scott A Burr, Donald H. Trust, Trevor J Pavlovskis, Olgerts R Guerry, Patricia (B) TITLE: Specific Detection of Campylobacter jejuni and Campylobacter coli by Using Polymerase Chain Reaction (C) JOURNAL: J. Clin. Microbiol. (D) VOLUME: 30 (E) ISSUE: 10 (F) PAGES: 2613-2619 (G) DATE: October-1992 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: ATGGGATTTCGTATTAAC 18 (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: YES (vi) ORIGINAL SOURCE: (A) ORGANISM: Campylobacter coli (B) STRAIN: VC167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: GAACTTGAACCGATTTG17

| Full | Title | Citation | Front | Review | Classification | Date | Reference | | | Claims | KWIC | Draw. De |

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L3: Entry 12 of 12   File: USPT   Feb 27, 1996

DOCUMENT-IDENTIFIER: US 5494795 A
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DNA. The probe lies between base pairs 481-759 of the DNA in GenBank Accession No.
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Detailed Description Paragraph Table (2):

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L5: Entry 8 of 19   File: USPT   Oct 10, 2000

DOCUMENT-IDENTIFIER: US 6130082 A
TITLE: Recombinant flagellin vaccines

Abstract Text (1):
The present invention is directed to recombinant genes and their encoded proteins
which are recombinant flagellin fusion proteins. Such fusion proteins comprise amino
amino acid sequences specifying an epitope encoded by a flagellin structural gene
and an epitope of a heterologous organism which is immunogenic upon introduction of
the fusion protein into a vertebrate host. The recombinant genes and proteins of
the present invention can be used in vaccine formulations, to provide protection
against infection by the heterologous organism, or to provide protection against
conditions or disorders caused by an antigen of the organism. In a specific
embodiment, attenuated invasive bacteria expressing the recombinant flagellin genes
of the invention can be used in live vaccine formulations. The invention is
illustrated by way of examples in which epitopes of malaria circumsporozoite
antigens, the B subunit of Cholera toxin, surface and presurface antigens of
Hepatitis B. VP7 polypeptide of rotavirus, envelope glycoprotein of HIV, and M
protein of Streptococcus, are expressed in recombinant flagellin fusion proteins
which assemble into functional flagella, and which provoke an immune response
directed against the heterologous epitope, in a vertebrate host.

Brief Summary Text (16):
Cholera toxin is the prototype of a family of bacterial enterotoxins which mediate
diarrheal disease and are related in structure, function and immunogenicity. Other
members of this family include the heat-labile toxin of E. coli isolated from
humans (Yamamoto, T. and Yokota, T., 1983, J. Bacteriology 155:728) and from pigs
(Leong, J., et al., 1985, Infect. Immun. 48:73), and toxins from Salmonella
typhimurium (Finkelstein, R. A., et al., 1983, FEMS Microbiology Letters 17:239)
and from Campylobacter jejuni (Walker, R. I., et al., 1986, Microbiology Rev.
50:81). Common to all of these toxins is an A subunit which mediates ADP-
ribosyltransferase activity, resulting in the activation of adenylate cyclase,
ultimately leading to death of the target cell. In addition, all of these toxins
contain an immunologically dominant B subunit which mediates binding of the
holotoxin to the target cell. The B subunit by itself is non-toxic, and
immunization with this molecule induces the formation of toxin-neutralizing
antibodies.

Brief Summary Text (23):
Flagella are found primarily, although not exclusively, on the surface of rod and
spiral shaped bacteria, including members of the genera Escherichia, Salmonella,
Proteus, Pseudomonas, Bacillus, Campylobacter, Vibrio, Treponema, Legionella,
Clostridia, Caulobacter, and others. These flagella, although they perform the same
function, are polymorphic in molecular weight across genera, ranging from 28-66 kd.
A high degree of antigenic polymorphism is seen even within a single genus, such as
Salmonella, and is useful for identifying individual serotypes within a single
species (Edwards, P. R. and Ewing, W. H., 1972, Identification of
Enterobacteriaceae, 3d ed., Burgess Publishing Co., Minneapolis, Minn.). Structural
analyses of several bacterial flagella have revealed a common architecture among

filaments isolated from different bacteria (Wei, L.-N. and Joys, T. M., 1985, J. Mol. Bio. 186:791; DeLange, R. J., et al., 1976, J. Biol. Chem. 251:705; Gill, P. R. R. and Agabian, J., Biol. Chem. 258:7395). Most striking is a high degree of protein protein sequence homology at the amino and carboxy termini of these molecules, and the presence of a polymorphic central region which is responsible for the antigenic diversity among different flagella.

Detailed Description Text (17):
If the cloned flagellin gene is not readily available, it may be cloned by standard procedures known in the art (see, e.g., Maniatis, T., et al., 1982, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York), with any flagellated bacterial cell potentially serving as the nucleic acid source for the molecular cloning. Such bacteria include but are not limited to Escherichia, Salmonella, Proteus, Pseudomonas, Bacillus, Campylobacter, Vibrio, Treponema, Legionella, Clostridia, and Caulobacter.

Detailed Description Text (53):
In a specific embodiment, any attenuated bacterial hosts which express the recombinant flagellin can be formulated as live vaccines. Such bacteria include but are not limited to attenuated invasive strains and attenuated Campylobacter, Shigella or Escherichia species.

CLAIMS:

1. A recombinant gene comprising a nuclcotide sequence which encodes a flagellin fusion protein, which protein comprises a flagellin sequence containing a first epitope of a Salmonella H1-d flagellin structural gene with at least one epitope of a heterologous organism inserted within the flagellin sequence, wherein the flagellin protein is capable of binding to an antiflagellin antibody, wherein the DNA encoding at least one epitope of the heterologous organism is inserted in place of the DNA which naturally occurs between the natural EcoRV sites of the Salmonella H1-d gene.

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The SIB BLAST network service uses a server developed at SIB and the NCBI
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W.,
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query length: 575 AA (of which 9% low-complexity regions filtered out)
Date run: 2004-08-31 17:39:24 UTC+0100 on sib-gm1.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
          1,544,870 sequences; 494,584,931 total letters

| Taxonomic view | NiceBlast view | Printable view |

List of potentially matching sequences

Send selected sequences to | Clustal W (multiple alignment) ▼ | **Submit Query** |
| Select up to... |

☐ Include query sequence

```
    Db AC       Description                                              Score E-value

☐ sp P22251 FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]          983   0.0
☐ tr O85179 Flagellin A [flaA] [Campylobacter jejuni]                     983   0.0
☐ tr Q9R950 Flagellin A [flaA] [Campylobacter jejuni]                     979   0.0
☐ tr Q9R953 Flagellin A [flaA] [Campylobacter jejuni]                     979   0.0
☐ tr Q9RF26 Chimeric flagellin A/B [Campylobacter jejuni]                 977   0.0
☐ tr O85183 Flagellin A [flaA] [Campylobacter jejuni]                     957   0.0
☐ tr Q8G9F3 Flagellin (Fragment) [flaA] [Campylobacter coli]              956   0.0
☐ tr Q7X516 FlaB [flaB] [Campylobacter jejuni]                            935   0.0
☐ tr Q9RF25 Flagellin B [flaB] [Campylobacter jejuni]                     934   0.0
☐ sp P22252 FLB2_CAMJE Flagellin B [flaB] [Campylobacter jejuni]          932   0.0
```

☐	tr	Q9RPY6	Flagellin A [flaA] [Campylobacter jejuni]	918	0.0
☐	tr	Q99Q27	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	905	0.0
☐	tr	Q99QL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	905	0.0
☐	tr	Q93NL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	875	0.0
☐	tr	Q93NL9	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	874	0.0
☐	sp	P27053	FLAA_CAMCO Flagellin A [flaA] [Campylobacter coli]	873	0.0
☐	tr	Q84IB9	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	863	0.0
☐	tr	Q46009	Flagellin [Campylobacter coli]	848	0.0
☐	sp	P18245	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campyloba...	837	0.0
☐	sp	Q46113	FLA3_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	803	0.0
☐	tr	Q84IB8	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	802	0.0
☐	tr	Q9R952	Flagellin A [flaA] [Campylobacter jejuni]	801	0.0
☐	sp	P56963	FLA1_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	800	0.0
☐	tr	O85182	Flagellin A [flaA] [Campylobacter jejuni]	796	0.0
☐	tr	Q9R949	Flagellin A [flaA] [Campylobacter jejuni]	796	0.0
☐	tr	O30696	Flagellin A [flaA] [Campylobacter jejuni]	795	0.0
☐	tr	O30689	Flagellin A [flaA] [Campylobacter jejuni]	794	0.0
☐	tr	Q8G9F2	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	793	0.0
☐	tr	O34938	Flagellin A [flaA] [Campylobacter jejuni]	792	0.0
☐	tr	O85180	Flagellin A [flaA] [Campylobacter jejuni]	785	0.0
☐	tr	Q8G9F1	Flagellin (Fragment) [flaA] [Campylobacter coli]	782	0.0
☐	sp	Q46114	FLB3_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	776	0.0
☐	tr	Q8G9F0	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	768	0.0
☐	tr	Q79AR6	Flagellin [flaA] [Campylobacter jejuni]	767	0.0
☐	sp	P56964	FLB1_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	766	0.0
☐	tr	Q6L5K6	Flagellin (Fragment) [flaA] [Campylobacter lari]	766	0.0
☐	tr	Q6L5J8	Flagellin (Fragment) [flaA] [Campylobacter lari]	765	0.0
☐	tr	Q9R951	Flagellin B [flaB] [Campylobacter jejuni]	763	0.0
☐	tr	Q933V4	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	762	0.0
☐	tr	Q6L5K1	Flagellin (Fragment) [flaA] [Campylobacter lari]	762	0.0
☐	tr	Q9R954	Flagellin B [flaB] [Campylobacter jejuni]	761	0.0
☐	tr	Q6L5J9	Flagellin (Fragment) [flaA] [Campylobacter lari]	761	0.0
☐	tr	Q93NL8	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	760	0.0
☐	tr	Q93NL7	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	756	0.0
☐	tr	Q6L5K5	Flagellin (Fragment) [flaA] [Campylobacter lari]	756	0.0
☐	tr	Q6L5K8	Flagellin (Fragment) [flaA] [Campylobacter lari]	755	0.0
☐	tr	Q6L5J7	Flagellin (Fragment) [flaA] [Campylobacter lari]	755	0.0
☐	tr	Q6L5K2	Flagellin (Fragment) [flaA] [Campylobacter lari]	754	0.0
☐	tr	Q6L5K9	Flagellin (Fragment) [flaA] [Campylobacter lari]	754	0.0
☐	tr	Q6L5L0	Flagellin (Fragment) [flaA] [Campylobacter lari]	754	0.0
☐	tr	Q6L5K4	Flagellin (Fragment) [flaA] [Campylobacter lari]	751	0.0
☐	tr	Q6L5K7	Flagellin (Fragment) [flaA] [Campylobacter lari]	751	0.0
☐	tr	Q6L5J6	Flagellin (Fragment) [flaA] [Campylobacter lari]	749	0.0
☐	tr	Q6L5L1	Flagellin (Fragment) [flaA] [Campylobacter lari]	747	0.0
☐	tr	O85181	Flagellin B [flaB] [Campylobacter jejuni]	747	0.0

☐	tr	Q6L5K0	Flagellin (Fragment) [flaA] [Campylobacter lari]	746	0.0
☐	tr	Q6L5K3	Flagellin (Fragment) [flaA] [Campylobacter lari]	742	0.0
☐	tr	P96751	Flagellin (Fragment) [flaA] [Campylobacter sp]	605	e-172
☐	tr	P96752	Flagellin [flaB] [Campylobacter sp]	598	e-169
☐	tr	Q84IC4	Flagellin (Fragment) [flaA] [Campylobacter lari]	537	e-151
☐	tr	Q84IC5	Flagellin (Fragment) [flaA] [Campylobacter lari]	534	e-150
☐	tr	Q84IC7	Flagellin (Fragment) [flaA] [Campylobacter lari]	523	e-147
☐	tr	Q84IC8	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-134
☐	tr	Q93GT4	Flagellin (Fragment) [flaA] [Campylobacter lari]	476	e-133
☐	tr	Q8RTY4	Flagellin (Fragment) [flaA] [Campylobacter lari]	475	e-132
☐	tr	Q56746	Flagellin [flag] [Wolinella succinogenes]	474	e-132
☐	tr	Q93R24	Flagellin (Fragment) [flaA] [Campylobacter lari]	474	e-132
☐	tr	Q7M7N1	FLAGELLIN B [FLAB] [Wolinella succinogenes]	473	e-132
☐	tr	Q84IC9	Flagellin (Fragment) [flaA] [Campylobacter lari]	471	e-131
☐	tr	Q93GT1	Flagellin (Fragment) [flaA] [Campylobacter lari]	469	e-131
☐	tr	Q84IC3	Flagellin (Fragment) [flaA] [Campylobacter lari]	469	e-131
☐	tr	Q84IC6	Flagellin (Fragment) [flaA] [Campylobacter lari]	468	e-130
☐	tr	Q84IC2	Flagellin (Fragment) [flaA] [Campylobacter lari]	466	e-130
☐	tr	Q93GT2	Flagellin (Fragment) [flaA] [Campylobacter lari]	462	e-129
☐	tr	Q84IC1	Flagellin (Fragment) [flaA] [Campylobacter lari]	462	e-129
☐	tr	Q93GT3	Flagellin (Fragment) [flaA] [Campylobacter lari]	456	e-127
☐	tr	Q46462	Flagellin (Fragment) [fla2] [Campylobacter upsaliensis]	451	e-125
☐	tr	Q46461	Flagellin (Fragment) [fla1] [Campylobacter upsaliensis]	446	e-124
☐	sp	Q9XB38	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	444	e-123
☐	tr	Q7X2D1	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...	443	e-123
☐	sp	Q03843	FLAA_HELPY Flagellin A [flaA] [Helicobacter pylori (Ca...	438	e-121
☐	tr	Q8GD49	Flagellin [flaB] [Helicobacter pylori (Campylobacter p...	434	e-120
☐	tr	Q6VYQ2	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...	433	e-120
☐	tr	Q84IC0	Flagellin (Fragment) [flaA] [Campylobacter lari]	412	e-114
☐	tr	Q8VN90	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...	383	e-105
☐	tr	Q8VN91	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...	382	e-105
☐	tr	Q8VLN3	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...	382	e-105
☐	sp	Q07910	FLAB_HELMU Flagellin B (Flagellin N) [flaB] [Helicobac...	381	e-104
☐	tr	Q7X2D0	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...	380	e-104
☐	tr	Q8RNU8	Flagellin B subunit [flaB] [Helicobacter pylori (Campy...	378	e-103
☐	sp	Q07911	FLAB_HELPY Flagellin B (Flagellin N) [flaB] [Helicobac...	377	e-103
☐	sp	Q9ZMV8	FLAB_HELPJ Flagellin B (Flagellin N) [flaB] [Helicobac...	377	e-103
☐	tr	Q6VYQ1	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...	377	e-103
☐	tr	Q9XB37	Flagellin B [flaB] [Helicobacter felis]	373	e-102
☐	tr	Q7TTM9	Major flagellin subunit FlaA_1 (Major flagellin subuni...	368	e-100
☐	tr	Q7VF81	Minor flagellin subunit FlaB [flaB] [Helicobacter hepa...	357	4e-97
☐	sp	P50612	FLAA_HELMU Flagellin A [flaA] [Helicobacter mustelae]	345	1e-93
☐	tr	Q93NM1	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	337	4e-91
☐	tr	Q93NM0	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	337	4e-91
☐	tr	Q8VN93	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...	337	5e-91

Graphical overview of the alignments

| Click here | to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits   Flagellin_N   Flagell Flagel   Flagelli

Matches on query sequence

Mat

Submission		Mat
	1 500	1
FLA2_CAMJE		
085179		
Q9R950		
Q9R953		
Q9RF26		
085183		
Q8G9F3		
Q7X516		
Q9RF25		
FLB2_CAMJE		
Q9RPY6		
Q99Q27		
Q99QL6		
Q93NL6		
Q93NL9		
FLAA_CAMCO		
Q84IB9		
Q46009		
FLAB_CAMCO		
FLA3_CAMJE		
Q84IB8		
Q9R952		
FLA1_CAMJE		
085182		
Q9R949		
O30696		
O30689		
Q8G9F2		
O34938		
085180		
Q8G9F1		
FLB3_CAMJE		
Q8G9F0		
Q79AR6		
FLB1_CAMJE		
Q6L5K6		
Q6L5J8		
Q9R951		
Q933V4		
Q6L5K1		
Q9R954		
Q6L5J9		
Q93NL8		
Q93NL7		
Q6L5K5		
Q6L5K8		
Q6L5J7		
Q6L5K2		
Q6L5K9		
Q6L5L0		
Q6L5K4		
Q6L5K7		
Q6L5J6		
Q6L5L1		
085181		
Q6L5K0		
Q6L5K3		
P96751		
P96752		
Q84IC4		
Q84IC5		
Q84IC7		
Q84IC8		
Q93GT4		
Q8RTY4		
Q56746		
Q93R24		
Q7M7N1		
Q84IC9		
Q93GT1		
Q84IC3		
Q84IC6		
Q84IC2		
Q93GT2		
Q84IC1		
Q93GT3		
Q46462		
Q46461		
FLAA_HELFE		
Q7X2D1		
FLAA_HELPY		
Q8GD49		
Q6VYQ2		
Q84IC0		
Q8VN90		
Q8VN91		

Alignments

```
sp      P22251          Flagellin A [flaA] [Campylobacter jejuni]  575 AA
        FLA2_CAMJE                                                 align
```

 Score = 983 bits (2542), Expect = 0.0
 Identities = 526/575 (91%), Positives = 526/575 (91%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 420

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KNL                   NTYVV              QFAALKTTAANTTDETAGVT
Sbjct: 421  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 480

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
```

```
tr      O85179          Flagellin A [flaA] [Campylobacter jejuni]  576 AA
                                                                   align
```

 Score = 983 bits (2542), Expect = 0.0
 Identities = 526/575 (91%), Positives = 526/575 (91%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQDSGFSRGSGFSVGS 421

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KNL                     NTYVV               QFAALKTTAANTTDETAGVT
Sbjct: 422  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 482  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 542  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 576
```

tr   Q9R950   **Flagellin A [flaA] [Campylobacter jejuni]**   576 AA
                                                                        align

Score = 979 bits (2532), Expect = 0.0
Identities = 524/575 (91%), Positives = 526/575 (91%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
```

```
             ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             YAIKEGTTSQ+FAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242  YAIKEGTTSQNFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
             ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
             SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 421

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
              KNL                    NTYVV                QFAALKTTAANTTDETAGVT
Sbjct: 422  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
             TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 482  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
             SESANYSKANILAQSGS+AMAQANSSQQNVLRLLQ
Sbjct: 542  SESANYSKANILAQSGSHAMAQANSSQQNVLRLLQ 576
```

```
tr    Q9R953        Flagellin A [flaA] [Campylobacter jejuni]      576 AA
                                                                    align
```

```
 Score =  979 bits (2530), Expect = 0.0
 Identities = 524/575 (91%), Positives = 525/575 (91%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNGAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIKEGTTSQ+FAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS
```

```
Sbjct: 242 YAIKEGTTSQEFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
           SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 421

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KNL                 NTYVV               QFAALKTTAANTTDETAGVT
Sbjct: 422 GKNLSVGLSQGIQIISSAGSMSNTYVVSAGSGFSSGSGSNSQFAALKTTAANTTDETAGVT 481

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
           TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 482 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 542 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 576
```

```
tr   Q9RF26       Chimeric flagellin A/B [Campylobacter jejuni]   576 AA
                                                                 align
```

```
Score = 977 bits (2526), Expect = 0.0
Identities = 522/575 (90%), Positives = 525/575 (90%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
           TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 182 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
           SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 421
```

```
Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KNL                     NTYVV              QFAALKTTAANTTDETAGVT
Sbjct: 422 GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481


Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 482 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541


Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 542 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 576
```

tr   O85183   **Flagellin A [flaA] [Campylobacter jejuni]**   576 AA
                                                                        align


```
Score = 957 bits (2475), Expect = 0.0
Identities = 509/575 (88%), Positives = 517/575 (89%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNV+ALNAK NSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQ NTL
Sbjct: 2    GFRINTNVSALNAKPNSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQTNTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQT+KATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIKEGTTSQ+FAINGV IG+I YKDGD NG L+SAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242  YAIKEGTTSQNFAINGVVIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 421

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KNL                     NTYVV              QF  LKTTAANTTDETAGVT
Sbjct: 422  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFGVLKTTAANTTDETAGVT 481

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMA MDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF+
Sbjct: 482  TLKGAMAGMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFS 541
```

```
Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSY+MAQANSSQQNVLRLLQ
Sbjct: 542 SESANYSKANILAQSGSYSMAQANSSQQNVLRLLQ 576
```

tr   Q8G9F3   **Flagellin (Fragment) [flaA] [Campylobacter coli]**   575 AA
                                                                          align

```
 Score = 956 bits (2471), Expect = 0.0
 Identities = 511/575 (88%), Positives = 519/575 (89%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKANSDLN+KSLD SL+RLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNGAALNAKANSDLNSKSLDQSLARLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSG FTNQEFQIGASSNQT+KATIGATQSSKIGVTRFETGAQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIKEGTTSQDFAINGVTIGKIEYKDGDG+GSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGDGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQISATNADAMGFNSYKGGGK V +  VSSISAFM
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGGKLVLSSAVSSISAFMSAQNSGFSRGSGFSVGS 420

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KNL                   NTYVV               QFAALKTTAANTTDETAGVT
Sbjct: 421 GKNLSVGLNQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 480

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMD+AETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 481 TLKGAMAVMDMAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
```

tr   Q7X516   **FlaB [flaB] [Campylobacter jejuni]**   576 AA
                                                            align

```
Score = 935 bits (2417), Expect = 0.0
Identities = 497/575 (86%), Positives = 510/575 (88%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN+ ALNA ANS +N+  LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2    GFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIKEGTTSQDFAINGV IG+I YKDGD NG L+SAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242  YAIKEGTTSQDFAINGVAIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 421

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KNL                   NTYVV              QFAALKTTAANTTDETAGVT
Sbjct: 422  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA
Sbjct: 482  TLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 541

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 542  SESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 576
```

tr Q9RF25   **Flagellin B [flaB] [Campylobacter jejuni]**   576 AA
                                                                    align

```
Score = 934 bits (2413), Expect = 0.0
Identities = 495/575 (86%), Positives = 510/575 (88%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN+ ALNA ANS +N+  LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2    GFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
```

```
Sbjct:  62  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQT+KATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIKEGTTSQDFAINGV IG+I YKDGD NG L+SAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242  YAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 421

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KNL                    NTYVV               QFAALKTTAANTTDETAGVT
Sbjct: 422  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA
Sbjct: 482  TLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 541

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 542  SESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 576
```

sp   P22252   **Flagellin B [flaB] [Campylobacter jejuni]**   575 AA
       FLB2_CAMJE   align

```
 Score =  932 bits (2408), Expect = 0.0
 Identities = 494/575 (85%), Positives = 509/575 (87%)

Query:  1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN+ ALNA ANS +N+   LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct:  1   GFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQT+KATIGATQSSKIGVTRFETGAQSF
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV
Sbjct: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
```

```
Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKEGTTSQDFAINGV IG+I YKDGD NG L+SAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
           SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 420

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KNL               NTYVV              QFAALKTTAANTTDETAGVT
Sbjct: 421 GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 480

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
           TLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA
Sbjct: 481 TLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 540

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           SESAN+SK NILAQSGSYAM+Q N+ QQNVL+LLQ
Sbjct: 541 SESANFSKYNILAQSGSYAMSQRNAVQQNVLKLLQ 575
```

tr   Q9RPY6   **Flagellin A [flaA] [Campylobacter jejuni]**   574 AA
                                                                          align

```
 Score = 918 bits (2372), Expect = 0.0
 Identities = 489/575 (85%), Positives = 506/575 (87%), Gaps = 2/575 (0%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 181

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 241

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQDFAINGV IG+I Y DGD NG LISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKAGNTSQDFAINGVVIGQINYNDGDNNGQLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 359
```

```
Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
             SVSLRESKGQISA NADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 360  SVSLRESKGQISAANADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVGS 419


Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
              KNL                    NTYVV               QFAALKTTAANTTDETAGVT
Sbjct: 420  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 479


Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
             TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 480  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 539


Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
             SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 540  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 574
```

tr Q99Q27   **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 576 AA
                                                                            align


```
 Score =  905 bits (2340), Expect = 0.0
 Identities = 484/576 (84%), Positives = 501/576 (86%), Gaps = 1/576 (0%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKANSDLNAKSLD+SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60


Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120


Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSF
Sbjct: 121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180


Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINK+ADKTGVRATYDVKTTG
Sbjct: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGA 240


Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIK GTTSQDFAINGV IGK++YKDGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241  YAIKAGTTSQDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTS 300


Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGIL+ QKENYGRLSLVKNDGRDIN+SGT LSAIGMG  DMISQ+
Sbjct: 301  ADGRGIKITGDIGVGSGILSAQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQA 360


Query: 361  SVSLRESKGQISATNADAMGFNSYKGGG-KFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 419
            SVSLRESKGQISA NADAMGFNSY GGG K +        SSISAFM
Sbjct: 361  SVSLRESKGQISAANADAMGFNSYNGGGAKQILQVQASSISAFMSQAGSGFSAGSGFSAG 420


Query: 420  XXKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGV 479
              K                       +TYV+               QFAALKT+  +  + TAGV
Sbjct: 421  SGKGYSTILSGSVQIVSSTASMSSTYVISAGSGFSVGSGNSQFAALKTSTVSAHEATAGV 480


Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
```

```
            TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK+AESQIRDVDF
Sbjct: 481  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKSAESQIRDVDF 540

Query: 540  ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 541  ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 576
```

tr   Q99QL6   **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]**   574 AA
align

Score = 905 bits (2338), Expect = 0.0
Identities = 484/575 (84%), Positives = 500/575 (86%), Gaps = 1/575 (0%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKANSDLNAKSLD+SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSF
Sbjct: 121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINK+ADKTGVRATYDVKTTG
Sbjct: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIK GTTSQDFAINGV IGK++YKDGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241  YAIKAGTTSQDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIKITGDIGVGSGIL+ QKENYGRLSLVKNDGRDIN+SGT LSAIGMG  DMISQ+
Sbjct: 301  ADGRGIKITGDIGVGSGILSTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQISA NADAMGFNSY GGG    Q SSISAFM
Sbjct: 361  SVSLRESKGQISAANADAMGFNSYNGGGAKQILQ-ASSISAFMSQAGSGFSAGSGFSAGS 419

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             K                      +TYV+              QFAALKT+  +   + TAGVT
Sbjct: 420  GKGYSTILSGSVQIVSSTASMSSTYVISEGSGFSAGSGNSQFAALKTSTVSAHEATAGVT 479

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK+AESQIRDVDFA
Sbjct: 480  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKSAESQIRDVDFA 539

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 540  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 574
```

```
tr    Q93NL6      Flagellin A (Fragment) [flaA] [Campylobacter jejuni]  557 AA
                                                                         align


 Score =  875 bits (2262), Expect = 0.0
 Identities = 468/558 (83%), Positives = 484/558 (85%), Gaps = 1/558 (0%)

Query:  10  ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
            ALNAKANSDLNAKSLD+SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct:   1  ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query:  70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
            ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT
Sbjct:  61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130  SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
            SFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSFTSGVVGLTI
Sbjct: 121  SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGVVGLTI 180

Query: 190  KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTS 249
            KNYNGIEDFKFDNVVISTSVGTGLGALAEEINK+ADKTGVRATYDVKTTG YAIK GTTS
Sbjct: 181  KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250  QDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
            QDFAINGV IGK++YKDGD NGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT
Sbjct: 241  QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 300

Query: 310  GDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
            GDIGVGSGIL+ QKENYGRLSLVKNDGRDIN+SGT LSAIGMG  DMISQ+SVSLRESKG
Sbjct: 301  GDIGVGSGILSTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQASVSLRESKG 360

Query: 370  QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
            QISA NADAMGFNSY GGG    Q  SSISAFM                     K
Sbjct: 361  QISAANADAMGFNSYNGGGAKQILQ-ASSISAFMSQAGSGFSAGSGFSAGSGKGYSTILS 419

Query: 430  XXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVM 489
                          +TYV+              QFAALKT+  +  + TAGVTTLKGAMAVM
Sbjct: 420  GSVQIVSSTASMSSTYVISEGSGFSAGSGNSQFAALKTSTVSAHEATAGVTTLKGAMAVM 479

Query: 490  DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKA 549
            DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK+AESQIRDVDFASESANYSKA
Sbjct: 480  DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKSAESQIRDVDFASESANYSKA 539

Query: 550  NILAQSGSYAMAQANSSQ 567
            NILAQSGSYAMAQANSSQ
Sbjct: 540  NILAQSGSYAMAQANSSQ 557




tr    Q93NL9      Flagellin A (Fragment) [flaA] [Campylobacter jejuni]  557 AA
                                                                         align


 Score =  874 bits (2259), Expect = 0.0
 Identities = 467/558 (83%), Positives = 484/558 (86%), Gaps = 1/558 (0%)

Query:  10  ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
            ALNAKANSDLNAKSLD+SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct:   1  ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60
```

```
Query:  70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
            ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT
Sbjct:  61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120


Query: 130  SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
            SFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSFTSG+VGLTI
Sbjct: 121  SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGIVGLTI 180


Query: 190  KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTS 249
            KNYNGIEDFKFDNVVISTSVGTGLGALAEEINK+ADKTGVRATYDVKTTG YAIK GTTS
Sbjct: 181  KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240


Query: 250  QDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
            QDFAINGV IGK++YKDGD NGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT
Sbjct: 241  QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 300


Query: 310  GDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
            GDIGVGSGIL QKENYGRLSLVKNDGRDIN+SGT LSAIGMG  DMISQ+SVSLRESKG
Sbjct: 301  GDIGVGSGILFTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQASVSLRESKG 360


Query: 370  QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
            QISA NADAMGFNSY GGG   Q SSISAFM                       K+
Sbjct: 361  QISAANADAMGFNSYNGGGAKQILQ-ASSISAFMSQAGSGFSAGSGFSAGSGKDYSTILS 419


Query: 430  XXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVM 489
                          +TYV+              QFAALKT+  +  + TAGVTTLKGAMAVM
Sbjct: 420  GSVQIVSSTASMSSTYVISEGSGFSAGSGNSQFAALKTSTVSAHEATAGVTTLKGAMAVM 479


Query: 490  DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKA 549
            DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK+AESQIRDVDFASESANYSKA
Sbjct: 480  DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKSAESQIRDVDFASESANYSKA 539


Query: 550  NILAQSGSYAMAQANSSQ 567
            NILAQSGSYAMAQANSSQ
Sbjct: 540  NILAQSGSYAMAQANSSQ 557
```


sp   P27053   **Flagellin A [flaA] [Campylobacter coli]**   572 AA
        FLAA_CAMCO   align


```
 Score =  873 bits (2256), Expect = 0.0
 Identities = 466/577 (80%), Positives = 495/577 (85%), Gaps = 7/577 (1%)

Query:   1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct:   1  GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60


Query:  61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct:  61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120


Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180


Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
```

```
                  +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 181  SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
                  YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241  YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
                  ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 301  ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXX 418
                  SVSLRESKGQISA NADAMGFN+Y GGG  + +F    SSI+ FM
Sbjct: 359  SVSLRESKGQISAANADAMGFNAYNGGGAKQIIF---ASSIAGFMSQAGSGFSAGSGFSV 415

Query: 419  XXXKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
                     KN                +TYVV                QFAAL+ +   + DETAG
Sbjct: 416  GSGKNYSAILSASIQIVSSARSISSTYVVSTGSGFSAGSGNSQFAALRISTVSAHDETAG 475

Query: 479  VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
                  VTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDVD
Sbjct: 476  VTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDVD 535

Query: 539  FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
                  FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 536  FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 572
```

tr   Q84IB9   **Flagellin (Fragment) [flaA] [Campylobacter jejuni]**   572 AA
                                                                              align

```
 Score = 863 bits (2229), Expect = 0.0
 Identities = 461/577 (79%), Positives = 491/577 (84%), Gaps = 7/577 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
                  GFRINTN AALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANT+
Sbjct: 1    GFRINTNGAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTM 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
                  GQAISNG+DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAISNGDDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
                  ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
                  +SG VGLTIKNYNGIEDFKF NVVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 181  SSGTVGLTIKNYNGIEDFKFQNVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
                  Y IK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241  YTIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
                  ADGRGIKITG IGVG+GIL    ENYGRLSLVKN GRDINISGT LSAIGMG TDMISQS
```

```
Sbjct: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNVGRDINISGTGLSAIGMGATDMISQS 358

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXX 418
           SVSLRESKGQISA NADAMGFN+Y GGG   + +F    SSI+ FM
Sbjct: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIF---ASSIAGFMSQAGSGFSAGSGFSV 415

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
              KN                  +TYVV                QFAAL+ +  +  DETAG
Sbjct: 416 GSGKNYSAILSASIQIVSSAASISSTYVVSAGSGFSAGSGNSQFAALRISTVSAHDETAG 475

Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
           VTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDVD
Sbjct: 476 VTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDVD 535

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 536 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 572
```

tr   Q46009   **Flagellin [Campylobacter coli]**   572 AA
                                                                   align

```
 Score = 848 bits (2191), Expect = 0.0
 Identities = 456/577 (79%), Positives = 487/577 (84%), Gaps = 8/577 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAAD ASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADVASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAA+DGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAEDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTR    + F
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRLNRFTK-F 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+D+K+ G
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDLKSVGA 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT  SAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGFSAIGMGATDMISQS 358

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXX 418
           SVSLRESKGQISA NADAMGFN+Y GGG   + +F    SSI+ FM
Sbjct: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIF---ASSIAGFMSQAGSGFSAGSGFSV 415

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
              KN                  +TYVV                QFAAL+ +  +  DETAG
Sbjct: 416 GSGKNYSAILSASIQIVSSAASISSTYVVSTGSGFSAGSGNSQFAALRISTVSAHDETAG 475
```

```
Query:  479  VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD  538
             VTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDVD
Sbjct:  476  VTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDVD  535


Query:  539  FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ  575
             FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct:  536  FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ  572
```

sp P18245   **Flagellin B (Flagellin N) [flaB] [Campylobacter coli]** 572 AA
    FLAB_CAMCO

                                                                    align

Score = 837 bits (2162), Expect = 0.0
Identities = 447/577 (77%), Positives = 482/577 (83%), Gaps = 7/577 (1%)

```
Query:  1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL  60
             GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct:  1    GFRINTNIGALNAHANSVVNARELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL  60

Query:  61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME  120
             GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct:  61   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME  120

Query:  121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF  180
             ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA IGATQSSKIGVTRFETG+QSF
Sbjct:  121  ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF  180

Query:  181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV  240
             +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct:  181  SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA  240

Query:  241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS  300
             YAIK G TSQDFAINGV IG+I Y DGD NG LISAINAVKDTTGVQASKDENGKLVLTS
Sbjct:  241  YAIKAGNTSQDFAINGVVIGQINYNDGDNNGQLISAINAVKDTTGVQASKDENGKLVLTS  300

Query:  301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS  360
             ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct:  301  ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS  358

Query:  361  SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXX  418
             SVSLRESKGQISA NADAMGFN+Y GGG + +F    SSI+ FM
Sbjct:  359  SVSLRESKGQISAANADAMGFNAYNGGGAKQIIF---ASSIAGFMSQAGSGFSAGSGFSV  415

Query:  419  XXXKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG  478
                KN                      +TYVV                QFAAL+ + + DETAG
Sbjct:  416  GSGKNYSAILSASIQIVSSARSISSTYVVSTGSGFSAGSGNSQFAALRISTVSAHDETAG  475

Query:  479  VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD  538
             VTTLKGAMAVMDIAETAITNLDQIRADIG++QNQ+  TINNITVTQVNVKAAES IRDVD
Sbjct:  476  VTTLKGAMAVMDIAETAITNLDQIRADIGAVQNQLQVTINNITVTQVNVKAAESTIRDVD  535

Query:  539  FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ  575
             FA+ESAN+SK NILAQSGSYAM+Q N+ QQNVL+LLQ
Sbjct:  536  FAAESANFSKYNILAQSGSYAMSQRNAVQQNVLKLLQ  572
```

```
sp      Q46113              Flagellin A [flaA] [Campylobacter jejuni]  574 AA
        FLA3_CAMJE                                                     align
```

Score = 803 bits (2075), Expect = 0.0
Identities = 437/578 (75%), Positives = 472/578 (81%), Gaps = 7/578 (1%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAI DSLRSQANTL
Sbjct: 1    GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIKDSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKA+IGATQSSKIG+TRFETG++
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKASIGATQSSKIGLTRFETGSRIS 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
              G V T+KNYNGI+DFKF  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181  VGGEVQFTLKNYNGIDDFKFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ G TS DFAINGV IGK++YKDGD NG+L+SAIN+VKDTTGV+AS DENGKL+LTS
Sbjct: 241  GAVRAGATSDDFAINGVKIGKVDYKDGDANGALVSAINSVKDTTGVEASIDENGKLLLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G+IG G+ I  N  ENYGRLSLVKNDG+DI ISGTNLSAIG GT +MISQ+
Sbjct: 301  REGRGIKIEGNIGRGAFINPNMLENYGRLSLVKNDGKDILISGTNLSAIGFGTGNMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQI A  ADAMGFNS   G            SS+SA+M
Sbjct: 361  SVSLRESKGQIDANVADAMGFNSANKGN---ILGGYSSVSAYMSSTGSGFSSGSGFSVGS 417

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
             KN                    Y V               QFA +KT+A NT    DETA
Sbjct: 418  GKNYSTGFANTIAISAASQLSA-VYNVSAGSGFSSGSNLSQFATMKTSAGNTLGVKDETA 476

Query: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
            GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 477  GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 536

Query: 538  DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 537  DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 574
```

```
tr      Q84IB8      Flagellin (Fragment) [flaA] [Campylobacter jejuni]  575 AA
                                                                        align
```

Score = 802 bits (2072), Expect = 0.0
Identities = 433/578 (74%), Positives = 471/578 (80%), Gaps = 6/578 (1%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG +
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181  TSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ G TS DFAINGV IGK++YKDGD NG+L SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 241  AAVRAGATSDDFAINGVKIGKVDYKDGDSNGALVSAINSVKDTTGVEASIDANGQLLLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISGTNLS+ G G T  ISQ+
Sbjct: 301  REGRGIKIDGNIGGGAFINASMKENYGRLSLVKNDGKDILISGTNLSSAGFGATQFISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQI A  ADAMGF S  G   V    SS++A+M
Sbjct: 361  SVSLRESKGQIDANIADAMGFGSVNKG---VMLGGFSSVTAYMSSAGSGFSAGSGYSVGS 417

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
             KN                 Y V           QFA +KT+A N+    DETA
Sbjct: 418  GKNYSTSISGIAVAFSSGSGLSAVYNVSAGSGFSSQSGLSQFATMKTSAGNSLGVKDETA 477

Query: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
            GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 537

Query: 538  DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            DFASESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538  DFASESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 575
```

tr   Q9R952   **Flagellin A [flaA] [Campylobacter jejuni]**   572 AA
                                                                     align

```
 Score = 801 bits (2068), Expect = 0.0
 Identities = 432/575 (75%), Positives = 470/575 (81%), Gaps = 4/575 (0%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
```

```
              ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
              +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
              A++ G TS DFAINGV IGK++YKDGD NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242  AAVRAGATSDDFAINGVKIGKVDYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
              +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct: 302  REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
              SVSLRESKGQI A  ADAMGF S    K V     SS+SA+M
Sbjct: 362  SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
               KN               Y V           QFA +KTTA    DETAGVT
Sbjct: 419  GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
              TLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478  TLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
              +ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538  AESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 572
```

```
sp    P56963              Flagellin A [flaA] [Campylobacter jejuni]  571 AA
      FLA1_CAMJE                                                       align
```

```
Score = 800 bits (2065), Expect = 0.0
Identities = 432/575 (75%), Positives = 469/575 (81%), Gaps = 4/575 (0%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181  TSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
              A++ G TS  FAINGV IGK++YKDGD NG+L++AIN+VKDTTGV+AS D NG+L+LTS
```

```
Sbjct: 241  AAVRAGATSDTFAINGVKIGKVDYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct: 301  REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQI A  ADAMGF S    K V    SS+SA+M
Sbjct: 361  SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 417

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KN                    Y V           QFA +KTTA    DETAGVT
Sbjct: 418  GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 476

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 477  TLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 536

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            +ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 537  AESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 571
```

tr   O85182   **Flagellin A [flaA] [Campylobacter jejuni]**   572 AA
                                                                       align

```
Score =  796 bits (2057), Expect = 0.0
Identities = 431/575 (74%), Positives = 468/575 (80%), Gaps = 4/575 (0%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A++ G TS  FAINGV IGK++YKDGD NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242  AAVRAGATSDTFAINGVKIGKVDYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct: 302  REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQI A  ADAMGF S    K V    SS+SA+M
Sbjct: 362  SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418
```

```
Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KN                      Y V             QFA  KTTA   DETAGVT
Sbjct: 419  GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATKKTTAFGVKDETAGVT 477


Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
             TLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478  TLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537


Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
             +ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538  AESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 572
```

tr   Q9R949   **Flagellin A [flaA] [Campylobacter jejuni]**   572 AA
                                                                      align


```
 Score = 796 bits (2055), Expect = 0.0
 Identities = 429/575 (74%), Positives = 468/575 (80%), Gaps = 4/575 (0%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
             GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61


Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
             GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121


Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
             ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181


Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 241


Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A++ G TS DFAINGV IGK++YKDGD NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242  AAVRAGATSDDFAINGVKIGKVDYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLTS 301


Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
             +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct: 302  REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 361


Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
             SVSLRESKG+  A ADAMGF S    K V   SS+SA+M
Sbjct: 362  SVSLRESKGRFDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418


Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KN                      Y V             QFA +KTTA   DETAGVT
Sbjct: 419  GKN-YSTGFAKAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477


Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
             TLKGAMAVMDIAETA TNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478  TLKGAMAVMDIAETATTNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537
```

```
Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            +ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538 AESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 572
```

tr   O30696   **Flagellin A [flaA] [Campylobacter jejuni]**   576 AA
                                                                        align

```
 Score =  795 bits (2053), Expect = 0.0
 Identities = 429/578 (74%), Positives = 471/578 (81%), Gaps = 6/578 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQA+IN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQANINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSF+GKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIANTTSFSGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGERIS 181

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V  T+KNYNGI+DFKF  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFKFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 241

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ GTTS DFAINGV IGK++YKDGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDDFAINGVKIGKVDYKDGDSNGALVSAINSVKDTTGVEASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T   SQ+
Sbjct: 302 REGRGIKIEGNIGGGAFINASMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFTSQA 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQI A  ADAMGF S  G K        S+++A+M
Sbjct: 362 SVSLRESKGQIDANIADAMGFGSVNKGVKL---SGFSTVTAYMSSAGSGFSAGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
             KN                  Y V            QFA +KT+ N+     DETA
Sbjct: 419 GKNYSTSISGIAVAFSSGSGLSAEYNVSAGSGFSSQSGLSQFATMKTSVGNSLGVKDETA 478

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
            GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 479 GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 538

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 539 DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 576
```

tr   O30689   **Flagellin A [flaA] [Campylobacter jejuni]**   572 AA
                                                                        align

```
Score = 794 bits (2050), Expect = 0.0
Identities = 428/575 (74%), Positives = 467/575 (80%), Gaps = 4/575 (0%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIAD+LRSQANTL
Sbjct: 2    GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADTLRSQANTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  TSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A++ G TS  FAINGV IGK++YKDGD NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242  AAVRAGATSDTFAINGVKIGKVDYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct: 302  REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQI A  ADAMGF S    K V     SS+SA+M
Sbjct: 362  SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KN                Y V           QFA +KTTA    DETAGVT
Sbjct: 419  GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETA TNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478  TLKGAMAVMDIAETATTNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            +ESANYSKANILAQSGSYAMAQANS  QNVLRLLQ
Sbjct: 538  AESANYSKANILAQSGSYAMAQANSVHQNVLRLLQ 572
```

tr Q8G9F2   **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 574 AA
                                                                    align

```
Score = 793 bits (2049), Expect = 0.0
Identities = 430/578 (74%), Positives = 469/578 (80%), Gaps = 7/578 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
```

```
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V  T+KNYNGI+DFKF  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181  SSGEVQFTLKNYNGIDDFKFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ GTTS+DF INGV IG+IEYKDGD NG+L++AIN+VKDTTGV+AS D NGKL+LTS
Sbjct: 241  GAVRAGTTSEDFTINGVKIGQIEYKDGDSNGALVAAINSVKDTTGVEASIDSNGKLLLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI GDIG G+ I  + KENYGRLSLVKNDG+DI ISG+NLS+ G G  + ISQ+
Sbjct: 301  REGRGIKIEGDIGRGAFINPDMKENYGRLSLVKNDGKDILISGSNLSSAGFGANNFISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQ+ A  ADAMGFNS   G            SS+ A+M
Sbjct: 361  SVSLRESKGQLDANVADAMGFNSVDKGN---ILGGYSSVQAYMSSAGSFSSGSGYSVGS 417

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
             KN                    Y +             QFA +KT+A N+      DETA
Sbjct: 418  GKNYSTGFANVVAVSAISQMSA-VYNISAGSGFSSGSTLSQFATMKTSAGNSLGVKDETA 476

Query: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
            GVTTLKGAMAVMDI ETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 477  GVTTLKGAMAVMDIPETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 536

Query: 538  DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            DFASESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 537  DFASESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 574
```

tr   O34938   **Flagellin A [flaA] [Campylobacter jejuni]**   575 AA
                                                                        align

```
Score = 792 bits (2045), Expect = 0.0
Identities = 428/578 (74%), Positives = 467/578 (80%), Gaps = 7/578 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKANSDLN+K+LD SL+RLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 2    GFRINTNVAALNAKANSDLNSKALDQSLARLSSGLRINSAADDASGMAIADSLRSQASTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVK TIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKTTIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             SG V  T+KNYNGI+DFKF  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  ESGEVQFTLKNYNGIDDFKFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 241
```

```
Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++EGTTS DF INGV IGK+EYKDGD NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 GAVREGTTSDDFTINGVKIGKVEYKDGDSNGALVAAINSVKDTTGVEASIDVNGQLLLTS 301


Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI GDIG G+ I  N KENYGRLSLVKNDG+DI ISGT L+A G G   ISQ+
Sbjct: 302 REGRGIKIEGDIGRGAFINPNMKENYGRLSLVKNDGKDILISGTGLTATGFGVNSFISQA 361


Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQI A  ADAMGFNS   G          SS+S++M
Sbjct: 362 SVSLRESKGQIDANVADAMGFNSVDKGN---ILGGFSSVSSYMSSAGSGFSSGSGFSVGS 418


Query: 421 XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
            KN                    Y +              QFA +KT+ NT   DETA
Sbjct: 419 GKNYSTGFANVVVVSAISQMSA-VYNISAGSGFSSQSGLSQFATMKTSVGNTLGVKDETA 477


Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
            GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDV
Sbjct: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDV 537


Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            DFA+ESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 538 DFAAESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
```

tr   O85180   **Flagellin A [flaA] [Campylobacter jejuni]**   575 AA
                                                                     <u>align</u>

Score = 785 bits (2027), Expect = 0.0
Identities = 425/578 (73%), Positives = 464/578 (79%), Gaps = 7/578 (1%)

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61


Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121


Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181


Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 241


Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ GTTS DFAINGV IGK+ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDDFAINGVKIGKVAYEDGDANGALVSAINSVKDTTGVEASIDANGQLLLTS 301


Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G IG G+ I  +   ENYGRLSLVKNDG+DI+ISGT LS  G G ++ ISQ
Sbjct: 302 REGRGIKIEGSIGGGAFINKDMMENYGRLSLVKNDGKDISISGTGLSFTGFGASNFISQV 361
```

```
Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQ+ A  ADAMGF S   G              SSI+ +M
Sbjct: 362  SVSLRESKGQLDANTADAMGFGSVNKG----LVLAASSIADYMSAEGSGFSAGSGYSVGS 417


Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
             K                          Y V              QFA +KT+A N+    DETA
Sbjct: 418  GKGYSATLTANAIAISSASAISKIYNVSQGSGFSSGSTLSQFATMKTSAGNSLGAKDETA 477


Query: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
            GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 537


Query: 538  DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538  DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 575
```


tr   <u>Q8G9F1</u>   **Flagellin (Fragment) [flaA] [Campylobacter coli]**   574 AA
                                                                          <u>align</u>

 Score = 782 bits (2020), Expect = 0.0
 Identities = 424/578 (73%), Positives = 463/578 (79%), Gaps = 7/578 (1%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60


Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120


Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 180


Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 240


Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A++ GTTS  FAINGV IGK+ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 241  AAVRAGTTSDTFAINGVKIGKVAYEDGDANGALVSAINSVKDTTGVEASIDANGQLLLTS 300


Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G IG G+ I +  ENYGRLSLVKNDG+DI+SGT LS  G G ++ ISQ
Sbjct: 301  REGRGIKIEGSIGGGAFINKDMMENYGRLSLVKNDGKDISISGTGLSFTGFASNFISQV 360


Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKGQ+ A  ADAMGF S   G              SSI+ +M
Sbjct: 361  SVSLRESKGQLDANTADAMGFGSVNKG----LVLAASSIADYMSAEGSGFSAGSGYSVGS 416


Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
             K                          Y V              QFA +KT+A N+    DETA
Sbjct: 417  GKGYSTTLTANAIAISSASAISKIYNVSQGSGFSSGSTLSQFATMKTSAGNSLGAKDETA 476


Query: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
```

```
                   GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 477   GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 536

Query: 538   DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
                   DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 537   DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 574
```

```
sp     Q46114              Flagellin B [flaB] [Campylobacter jejuni]   574 AA
       FLB3_CAMJE                                                       align

  Score = 776 bits (2005), Expect = 0.0
  Identities = 422/578 (73%), Positives = 464/578 (80%), Gaps = 7/578 (1%)

Query: 1     GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
                   GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1     GFRINTNIGALNAHANSVVNARELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61    GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
                   GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61    GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121   ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
                   ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG++
Sbjct: 121   ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGSRIS 180

Query: 181   TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
                    G V  T+KNYNGI+DFKF  VVISTSVGTGLGALAEEINKSAD+TGVRAT+ V+T G+
Sbjct: 181   VGGEVQFTLKNYNGIDDFKFQKVVISTSVGTGLGALAEEINKSADQTGVRATFTVETRGM 240

Query: 241   YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
                    A++ G TS+DFAINGV IG+IEYKDG NG+L+SAIN+VKDTTGV+AS DENGKL+LTS
Sbjct: 241   GAVRAGATSEDFAINGVKIGQIEYKDGDANGALVSAINSVKDTTGVEASIDENGKLLLTS 300

Query: 301   ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
                    +GRGIKI G+IG G+ I N  ENYGRLSLVKNDG+DI ISGTNLSAIG GT +MISQ+
Sbjct: 301   REGRGIKIEGNIGRGAFINPNMLENYGRLSLVKNDGKDILISGTNLSAIGFGTGNMISQA 360

Query: 361   SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
                   SVSLRESKGQI A  ADAMGFNS  G         SS+SA+M
Sbjct: 361   SVSLRESKGQIDANVADAMGFNSANKGN---ILGGYSSVSAYMSSTGSFSSGSGFSVGS 417

Query: 421   XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
                    KN                  Y V          QFA +KT+A NT    DETA
Sbjct: 418   GKNYSTGFANTIAISAASQLSA-VYNVSAGSGFSSGSNLSQFATMKTSAGNTLGVKDETA 476

Query: 478   GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
                   GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDV
Sbjct: 477   GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDV 536

Query: 538   DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
                   DFA+ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 537   DFAAESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 574
```

```
tr    Q8G9F0       Flagellin (Fragment) [flaA] [Campylobacter jejuni]  571 AA
                                                                        align
```

Score = 768 bits (1983), Expect = 0.0
Identities = 415/575 (72%), Positives = 457/575 (79%), Gaps = 4/575 (0%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1    GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ GTTS DFAINGV IG++EYKDGD NG+L++AIN+VKDTTGV+AS D NG+L+L+S
Sbjct: 241  AAVRAGTTSDDFAINGVKIGQVEYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLSS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G IG G+ I N  ENYGRLSLVKNDG+DI +SGT LS  G G    ISQ+
Sbjct: 301  REGRGIKIEGSIGRGAFINPNMMENYGRLSLVKNDGKDILVSGTGLSFAGFGANSFISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
            SVSLRESKG+  A  ADAMGF S  G   V       SS+SA+M
Sbjct: 361  SVSLRESKGRFDANTADAMGFGSVNKG---VMLAGYSSVSAYMSSAGSGFSSGSGYSVGS 417

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KN                   Y V             QFA +KTTA    DETAGVT
Sbjct: 418  GKNYSTGFANAIAIFSCSQLSA-VYNVSAGSGFSSQSGLSQFATMKTTAFGVKDETAGVT 476

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETA TNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA
Sbjct: 477  TLKGAMAVMDIAETATTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 536

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESAN+SK NILAQSGSYAM+QAN+ QQNVLRLLQ
Sbjct: 537  SESANFSKYNILAQSGSYAMSQANAVQQNVLRLLQ 571
```

```
tr    Q79AR6       Flagellin [flaA] [Campylobacter jejuni]      576 AA
                                                                 align
```

Score = 767 bits (1980), Expect = 0.0
Identities = 419/579 (72%), Positives = 459/579 (78%), Gaps = 8/579 (1%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61
```

```
Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A++ GTTS  FAINGV IGK+ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242  AAVRAGTTSDTFAINGVKIGKVAYEDGDANGALVSAINSVKDTTGVEASIDANGQLLLTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSL-VKNDGRDINISGTNLSAIGMGTTDMISQ 359
            +GRGIKI G IG G+ I +   ENYGRL   +K   +DI+ISGT LS  G G ++ ISQ
Sbjct: 302  REGRGIKIEGHIGGGAFINKDMIENYGRLLFWLKTTSKDISISGTGLSFTGFGASNFISQ 361

Query: 360  SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXX 419
            SVSLRESKGQ+ A  ADAMGF S   G           SSI+ +M
Sbjct: 362  VSVSLRESKGQLDANTADAMGFGSVNKG----LVLAASSIADYMSAEGSGFSAGSGYSVG 417

Query: 420  XXKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANT---TDET 476
              K                   Y V               QFA +KT+A N+    DET
Sbjct: 418  SGKGYSATLTANAIAISSASAISKIYNVSQGSGFSSGSTLSQFATMKTSAGNSLGAKDET 477

Query: 477  AGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRD 536
            AGVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRD
Sbjct: 478  AGVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRD 537

Query: 537  VDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            VDFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538  VDFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 576
```

sp   P56964   **Flagellin B [flaB] [Campylobacter jejuni]**   571 AA
      FLB1_CAMJE   align

 Score = 766 bits (1977), Expect = 0.0
 Identities = 412/575 (71%), Positives = 459/575 (79%), Gaps = 4/575 (0%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1    GFRINTNIGALNAHANSVVNARELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG +
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
```

```
              +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALAEEINKSADKTGVRAT+ V+T G+
Sbjct: 181 SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALAEEINKSADKTGVRATFTVETRGI 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
              A++ GTTS  FAINGVTIG++ Y+DGDGNG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 241 AAVRAGTTSDTFAINGVTIGQVAYEDGDGNGALVAAINSVKDTTGVEASIDANGQLLLTS 300

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
              +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct: 301 REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
              SVSLRESKG+  A  ADAMGF S    K V    SS+SA+M
Sbjct: 361 SVSLRESKGRFDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
               KN                   Y V          QFA +KTTA    DETAGVT
Sbjct: 418 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 476

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
              TLKGAMAVMDIAETA TNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA
Sbjct: 477 TLKGAMAVMDIAETATTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 536

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
              +ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 537 AESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 571
```

tr   Q6L5K6   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
                                                                    align

```
 Score = 766 bits (1977), Expect = 0.0
 Identities = 407/575 (70%), Positives = 462/575 (79%), Gaps = 7/575 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVA+LNA+AN++LN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSG FTNQEFQIG+ SNQ++KATIGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSQSNQSIKATIGATQSSKIGVTRFETGSMSN 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSG+  LTIKNYNGI+DFKF  VVISTSVGTG+GALAEEIN+ +D TGVRA + V+TTGV
Sbjct: 181 TSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEEINRVSDVTGVRANFLVETTGV 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             AIK   TSQDF+INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFSINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
             DGRGIKI G +G+G+G+L    ENYGRLSLVKNDG+DI ISGTNLS IGMG  DMISQ+
```

```
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDIAISGTNLSTIGMGAADMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
           S+SLRESKG I   ADAMGFN+YKGGGK + T   SS+S FM
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSTFMASENSGMSQGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KN+                    +              F A   AA   D+ AGVT
Sbjct: 419 GKNMSLVYNSTEALAFVTAF---SIAFGTGASTGGASQFANFVASANIAAK--DQQAGVT 473

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
           TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDFA
Sbjct: 474 TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDFA 533

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           +ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 534 AESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 568
```

tr Q6L5J8 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
                                                             align

```
 Score =  765 bits (1975), Expect = 0.0
 Identities = 407/575 (70%), Positives = 463/575 (79%), Gaps = 7/575 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+AN++LN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTT+FNGKQLLSG FTNQEFQIGA SNQ++KATIGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQEFQIGAQSNQSIKATIGATQSSKIGVTRFETGSMSN 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
           TSG+ LTIKNYNGI+DFKF VVISTSVGTG+GALAEEIN+ AD TGVRA + V+TTGV
Sbjct: 181 TSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEEINRVADVTGVRANFLVETTGV 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            AIK   TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            DGRGIKI G +G+G+G+L    ENYGRLSLVKNDG+DI ISG+NLS IGMG  DMISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDIAISGSNLSTIGMGAGDMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
           S+SLRESKG I   ADAMGFN+YKGGGK + T   SS+S+FM
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSSFMNSEGSGMSQGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KN+                    +              F A   AA   D+ AGVT
Sbjct: 419 GKNMSLVYNSTEALAFVTAF---SIAFGTGSSANGASQFANFVASANIAAK--DQQAGVT 473
```

```
Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
           TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDFA
Sbjct: 474 TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDFA 533


Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           +ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 534 AESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 568
```

tr   Q9R951   **Flagellin B [flaB] [Campylobacter jejuni]**   572 AA
                                                                            align

 Score = 763 bits (1971), Expect = 0.0
 Identities = 410/575 (71%), Positives = 459/575 (79%), Gaps = 4/575 (0%)

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN+ +LN+ ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2   GFRINTNIGSLNSHANSVVNARELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61


Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121


Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 181


Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
           +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALAEEINKSADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALAEEINKSADKTGVRATFTVETRGI 241


Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ GTTS  FAINGVTIG++ Y+DGDGNG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDTFAINGVTIGQVAYEDGDGNGALVAAINSVKDTTGVEASIDANGQLLLTS 301


Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct: 302 REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 361


Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
           SVSLRESKG+  A  ADAMGF S    K V      SS+SA+M
Sbjct: 362 SVSLRESKGRFDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418


Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KN                   Y V                QFA +KTTA    DETAGVT
Sbjct: 419 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477


Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
           TLKGAMAVMDIAETA TNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA
Sbjct: 478 TLKGAMAVMDIAETATTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 537


Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           +ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 538 AESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 572
```

```
tr   Q933V4      Flagellin A (Fragment) [flaA] [Campylobacter jejuni] 554 AA
                                                                      align


 Score =  762 bits (1968), Expect = 0.0
 Identities = 411/558 (73%), Positives = 447/558 (79%), Gaps = 4/558 (0%)

Query: 10   ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
            ALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1    ALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70   ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
            ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61   ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 120

Query: 130  SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
            SFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG + +SG V  T+
Sbjct: 121  SFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRISSSGEVQFTL 180

Query: 190  KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTS 249
            KNYNGI+DF+F  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+ A++ GTTS
Sbjct: 181  KNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGMAAVRAGTTS 240

Query: 250  QDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
             DF INGV IGK+EYKDGD NG+L++AIN+VKDTTGV+AS D NG+L+L+S +GRGIKI
Sbjct: 241  DDFTINGVKIGKVEYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLSSREGRGIKIE 300

Query: 310  GDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
            G IG G+ I N ENYGRLSLVKNDG+DI +SGT LS G G   ISQ+SVSLRESKG
Sbjct: 301  GSIGRGAFINPNMMENYGRLSLVKNDGKDILVSGTGLSFAGFGANSFISQASVSLRESKG 360

Query: 370  QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
            Q+ A ADAMGF S  G  V     SS+SA+M                    KN
Sbjct: 361  QLDANTADAMGFGSVNKG---VMLAGYSSVSAYMSSAGSGFSSGSGYSVGSGKNYSTGFA 417

Query: 430  XXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVM 489
                          Y V               QFA +KTTA    DETAGVTTLKGAMAVM
Sbjct: 418  NAIAISAASQLSA-VYNVSAGSGFSSQSGLSQFATMKTTAFGVKDETAGVTTLKGAMAVM 476

Query: 490  DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKA 549
            DIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA+ESANYSKA
Sbjct: 477  DIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFAAESANYSKA 536

Query: 550  NILAQSGSYAMAQANSSQ 567
            NILAQSGSYAMAQANS Q
Sbjct: 537  NILAQSGSYAMAQANSVQ 554




tr   Q6L5K1      Flagellin (Fragment) [flaA] [Campylobacter lari] 568 AA
                                                                  align


 Score =  762 bits (1967), Expect = 0.0
 Identities = 404/575 (70%), Positives = 463/575 (80%), Gaps = 7/575 (1%)


Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVA+LNA+AN++LN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
```

```
Sbjct: 1    GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLLSG FTNQEFQIG+ SNQ++KATIGATQSSKIGVTRFETG+ S
Sbjct: 121  ELDNIANTTAFNGKQLLSGGFTNQEFQIGSQSNQSIKATIGATQSSKIGVTRFETGSMSK 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             SG+ LTIKNYNGI+DFKF VVISTSVGTG+GALAEEIN+ AD TGVRA + V+TTGV
Sbjct: 181  DSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEEINRVADVTGVRANFLVETTGV 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            AIK   TSQDF+INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241  GAIKADKTSQDFSINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            DGRGIKI G +G+G+G+L    ENYGRLSLVKNDG+DI ISG+NLS IGMG T MISQ+
Sbjct: 301  RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDIAISGSNLSTIGMGATQMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            S+SLRESKG I   ADAMGFN+YKGGGK + T   SS+S+FM
Sbjct: 361  SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSSFMDSSGSGMSAGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KN+                    +              F   + AA   D+ AGVT
Sbjct: 419  GKNMSLVYNSTEALAFVTAF---SIAFGTGASTGWSSQSANFVTSASIAAK--DQQAGVT 473

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDFA
Sbjct: 474  TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDFA 533

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            +ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 534  AESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 568
```

tr   Q9R954   **Flagellin B [flaB] [Campylobacter jejuni]**   572 AA
                                                                        align

```
 Score = 761 bits (1966), Expect = 0.0
 Identities = 410/575 (71%), Positives = 457/575 (79%), Gaps = 4/575 (0%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN+  LNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2    GFRINTNIGPLNAHANSVVNARELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 181
```

```
Query:  181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SG V  T+KNYNGI+DF+F  VVISTSVGTGLGALAEEINKSADKTGVRAT+ V+T G+
Sbjct:  182 SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALAEEINKSADKTGVRATFTVETRGI 241

Query:  241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ GTTS  FAINGVTIG++ Y+DGDGNG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct:  242 AAVRAGTTSDTFAINGVTIGQVAYEDGDGNGALVAAINSVKDTTGVEASIDANGQLLLTS 301

Query:  301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +GRGIKI G+IG G+ I A+ KENYGRLSLVKNDG+DI ISG+NLS+ G G T  ISQ+
Sbjct:  302 REGRGIKIDGNIGGGAFINADMKENYGRLSLVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query:  361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKG+  A ADAMGF S    K V      SS+SA+M
Sbjct:  362 SVSLRESKGRFDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418

Query:  421 XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             KN                   Y V            QFA +KTTA    DETAGVT
Sbjct:  419 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477

Query:  481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAET  TNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA
Sbjct:  478 TLKGAMAVMDIAETDTTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 537

Query:  541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            +ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct:  538 AESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 572
```

tr   Q6L5J9   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   568 AA
                                                                       align

```
 Score =  761 bits (1965), Expect = 0.0
 Identities = 405/575 (70%), Positives = 462/575 (79%), Gaps = 7/575 (1%)

Query:  1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVA+LNA+AN++LN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct:  1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query:  61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct:  61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query:  121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLLSG FTNQEFQIGA SNQ++KATIGATQSSKIGVTRFETG+ S
Sbjct:  121 ELDNIANTTAFNGKQLLSGGFTNQEFQIGAQSNQSIKATIGATQSSKIGVTRFETGSMSN 180

Query:  181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             SG+  LTIKNYNGI+DFKF  VVISTSVGTG+GALAEEIN+ AD TGVRA + V+TTGV
Sbjct:  181 DSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEEINRVADVTGVRANFLVETTGV 240

Query:  241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            AIK   TSQ+F INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct:  241 GAIKADKTSQNFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300
```

```
Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            DGRGIKI G +G+G+G+L   ENYGRLSLVKNDG+DI ISG+NLS IGMG T MISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDILISGSNLSTIGMGATQMISQA 360


Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            S+SLRESKG I   ADAMGFN+YKGGGK + T   SS+S+FM
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSSFMASSGSGMSEGSGYSVNS 418


Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
            KN+                    +              F A   AA   D+ AGVT
Sbjct: 419 GKNMSLVYNSTEALAFVTAF---SIAFGTGSSANGRSQFANFVASANIAAK--DQQAGVT 473


Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDFA
Sbjct: 474 TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDFA 533


Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            +ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 534 AESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 568
```


tr   Q93NL8   **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 558 AA
                                                                              align

Score = 760 bits (1963), Expect = 0.0
Identities = 410/561 (73%), Positives = 451/561 (80%), Gaps = 6/561 (1%)

```
Query: 10  ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
            ALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60


Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
            ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 120


Query: 130 SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
            SFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG +  +SG V  T+
Sbjct: 121 SFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRISSSGEVQFTL 180


Query: 190 KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTS 249
            KNYNGI+DFKF  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+ A++ GTTS
Sbjct: 181 KNYNGIDDFKFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGMAAVRAGTTS 240


Query: 250 QDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
             DFAINGV IGK++YKDGD NG+L+SAIN+VKDTTGV+AS D NG+L+L+S +GRGIKI
Sbjct: 241 DDFAINGVKIGKVDYKDGDANGALVSAINSVKDTTGVEASIDANGQLLLSSREGRGIKIE 300


Query: 310 GDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
            G+IG G+ I  + KENYGRLSLVKNDG+DI ISG +LS+ G GTT  ISQ+SVSLRESKG
Sbjct: 301 GNIGGGAFINTDMKENYGRLSLVKNDGKDILISGNSLSSAGFGTTQFISQASVSLRESKG 360


Query: 370 QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
            QI A ADAMGF S  G   V    SS+SA+M                        KN
Sbjct: 361 QIDANIADAMGFGSVNKG---VVLGGYSSVSAYMSAEGSGFSAGSGYSVGSTKNYSATLS 417


Query: 430 XXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTD---ETAGVTTLKGAM 486
```

```
                                       Y V              QFA +KT+  N+       ETAGVTTLKGAM
Sbjct: 418 ANTITISAASQLSKVYNVSAGSGFSSQSGLSQFATMKTSVGNSLGVKAETAGVTTLKGAM 477

Query: 487 AVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANY 546
           AVMDIAETAITNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAESQIRDVDFA+ESANY
Sbjct: 478 AVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESQIRDVDFAAESANY 537

Query: 547 SKANILAQSGSYAMAQANSSQ 567
           SKANILAQSGSYAMAQANS Q
Sbjct: 538 SKANILAQSGSYAMAQANSVQ 558
```

tr   Q93NL7   **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]**   556 AA
                                                                          align

```
 Score = 756 bits (1953), Expect = 0.0
 Identities = 409/560 (73%), Positives = 450/560 (80%), Gaps = 6/560 (1%)

Query: 10  ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
           ALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
           ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 120

Query: 130 SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
           SFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG +  +SG V  T+
Sbjct: 121 SFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRISSSGEVQFTL 180

Query: 190 KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTS 249
           KNYNGI+DFKF  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+ A++ GTTS
Sbjct: 181 KNYNGIDDFKFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGMAAVRAGTTS 240

Query: 250 QDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
            DFAIN V IGK++YKDGD NG+L++AIN+VKDTTGV+AS D NG+L+LTS +GRGIKI
Sbjct: 241 DDFAINEVKIGKVDYKDGDANGALVAAINSVKDTTGVEASIDANGQLLLTSREGRGIKID 300

Query: 310 GDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
           G+IG G+ I + KENYGRLSLVKNDG+DI ISG +LS+ G GTT  ISQ+SVSLRESKG
Sbjct: 301 GNIGGGAFINTDMKENYGRLSLVKNDGKDILISGNSLSSAGFGTTQFISQASVSLRESKG 360

Query: 370 QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
           QI A  ADAMGF S  G          SS+SA+M                    KN
Sbjct: 361 QIDANIADAMGFGSVNKG----VVLGYSSVSAYMSAEGSGFSAGSGYSVGSTKNYSTVLT 416

Query: 430 XXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAA--NTTDETAGVTTLKGAMA 487
                        Y V             QFA +K +A   +   ETAGVTTLKGAMA
Sbjct: 417 ANAITISAASQLSKVYNVSAGSGFSSGSNLSQFATMKISAGAFDVKAETAGVTTLKGAMA 476

Query: 488 VMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYS 547
           VMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA+ESANYS
Sbjct: 477 VMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFAAESANYS 536

Query: 548 KANILAQSGSYAMAQANSSQ 567
           KA+ILAQSGSYAMAQANS Q
```

```
Sbjct: 537 KAHILAQSGSYAMAQANSVQ 556
```

tr   Q6L5K5   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 566 AA
align

```
 Score = 756 bits (1952), Expect = 0.0
 Identities = 404/576 (70%), Positives = 466/576 (80%), Gaps = 11/576 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLL G FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121  ELDNIANTTAFNGKQLLGGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SGV LTIKNYNGI+DFKF VVIS+SVGTG+GALAEEIN+ +D TGVRA + V+TTG
Sbjct: 181  SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVSDITGVRANFLVQTTGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            +IK   TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241  GSIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            DGRGI+ITG +G G+GIL +   +N+GRLSLVKNDG+DI ISG+NLSAIGMGT DMISQ+
Sbjct: 301  RDGRGIEITGSMGPGAGILKDDYKNFGRLSLVKNDGKDILISGSNLSAIGMGTADMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            S+SLRESKG I    ADAMGFN+YKGGGK V T  ++ISAFM
Sbjct: 361  SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FATISAFMSSAGSGMSAGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTA-ANTTDETAGV 479
            K++                 T                 QFAA T+A   D+ AGV
Sbjct: 419  GKDMSALYEGNLAFV-------TAFSVAFGFSAKNDGTSQFAAFATSANIAAKDQQAGV 470

Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
            TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 471  TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 531 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 566
```

tr   Q6L5K8   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
align

```
 Score = 755 bits (1950), Expect = 0.0
 Identities = 406/576 (70%), Positives = 463/576 (79%), Gaps = 10/576 (1%)
```

```
Query:   1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL  60
            GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct:   1  GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL  60

Query:  61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME  120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct:  61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME  120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF  180
            ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121  ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH  180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV  240
            +SGV  LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEIN+ AD TGVRA + V+TTG
Sbjct: 181  SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVQTTGA  240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS  300
            +IK   TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241  GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS  300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS  360
            DGRGI+ITG++GVGSG+L +   +N+GRLSLVKNDG+DI ISG+ LS IGMG  DMISQ+
Sbjct: 301  RDGRGIEITGNMGVGSGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA  360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX  420
            SVSLRESKG I    ADAMGFN+YKGGGK V T   SSI AFM
Sbjct: 361  SVSLRESKGNIDTHVADAMGFNAYKGGGKMVIT--FSSIEAFMSSNGSGMSAGSGFSIGS  418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV  479
             K +              T                 QFAA   TA+    D+ AGV
Sbjct: 419  GKEMSKIYNSGNLALV-------TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV  471

Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF  539
            TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472  TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF  531

Query: 540  ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ  575
            A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532  AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ  567
```

tr Q6L5J7   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 571 AA
                                                                    align

```
 Score =  755 bits (1950), Expect = 0.0
 Identities = 406/580 (70%), Positives = 464/580 (80%), Gaps = 14/580 (2%)

Query:   1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL  60
            GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct:   1  GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL  60

Query:  61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME  120
            GQAI+NGN ALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct:  61  GQAINNGNGALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME  120
```

```
Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            TSGV  LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEIN+ AD TGVRA + V+TTG
Sbjct: 181 TSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            +IK   TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            DGRGI+ITG++GVGSG+L +   +N+GRLSLVKNDG+DI ISG+ LS IGMG  DMISQ+
Sbjct: 301 RDGRGIEITGNMGVGSGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            S+SLRESKG I    ADAMGFN+YKGGGK V T   SSI AFM
Sbjct: 361 SISLRESKGNIDTHIADAMGFNAYKGGGKMVVT--FSSIEAFMSSDGSGMSAGSGFSIGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAANTT-----DE 475
            K +                    T                 QFAA  +A N +     D+
Sbjct: 419 GKEMSKIYNSGNLALV-------TAFSNAFGFSAKGDGASQFAAFAISAGNNSQIAAKDQ 471

Query: 476 TAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIR 535
            AGVTTLKGAMAVMDIAETAITNLDQIRADIG++QNQ+T+T+NNI+VTQVN+K+AES IR
Sbjct: 472 QAGVTTLKGAMAVMDIAETAITNLDQIRADIGAVQNQITATLNNISVTQVNIKSAESNIR 531

Query: 536 DVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            DVDFA+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532 DVDFAAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 571
```

tr   Q6L5K2   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
                                                                       align

```
Score =  754 bits (1948), Expect = 0.0
Identities = 405/576 (70%), Positives = 463/576 (80%), Gaps = 10/576 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SGV  LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEIN+ AD TGVRA + V+TTG
Sbjct: 181 SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
```

```
                  +IK    TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241  GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
                 DGRGI+ITG++GVGSG+L +  +N+GRLSLVKNDG+DI ISG+ LS IGMG  DMISQ+
Sbjct: 301  RDGRGIEITGNMGVGSGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
                 S+SLRESKG I    ADAMGFN+YKGGGK V T   SSI AFM
Sbjct: 361  SISLRESKGNIDTHIADAMGFNAYKGGGKMVVT--FSSIEAFMSSDGSGMSAGSGFSIGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
                 K +                 T                 QFAA   TA+    D+ AGV
Sbjct: 419  GKEMSKIYNSGNLALV-------TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV 471

Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
                 TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472  TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531

Query: 540  ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
                 A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532  AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 567
```

tr   Q6L5K9   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   567 AA
                                                                                    align

```
Score =  754 bits (1947), Expect = 0.0
Identities = 406/576 (70%), Positives = 462/576 (79%), Gaps = 10/576 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
                 GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
                 GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
                 ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A IGATQSSKIGVTRFETG+ S
Sbjct: 121  ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQAGIGATQSSKIGVTRFETGSMSH 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
                 +SGV  LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEIN+ AD TGVRA + V+TTG
Sbjct: 181  SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVQTTGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
                 +IK    TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241  GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
                 DGRGI+ITG++GVGSG+L +  +N+GRLSLVKNDG+DI ISG+ LS IGMG  DMISQ+
Sbjct: 301  RDGRGIEITGNMGVGSGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
                 SVSLRESKG I    ADAMGFN+YKGGGK V T   SSI AFM
```

```
Sbjct: 361  SVSLRESKGNIDTHVADAMGFNAYKGGGKMVIT--FSSIEAFMSSNGSGMSAGSGFSIGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
            K  +                     T                QFAA    TA+    D+ AGV
Sbjct: 419  GKEMSKIYNSGNLALV-------TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV 471

Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
            TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472  TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531

Query: 540  ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532  AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 567
```

tr   Q6L5L0   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 566 AA
                                                                        align

```
 Score =  754 bits (1946), Expect = 0.0
 Identities = 402/576 (69%), Positives = 466/576 (80%), Gaps = 11/576 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1    GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121  ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SGV  LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEIN+ +D TGVRA++ V+TTG
Sbjct: 181  SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVSDITGVRASFLVQTTGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             +IK   TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241  GSIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            +DGRGI+ITG +G GSG+L +    N+GRLSLVKNDG+DI ISG+NLSAIGMGT DMISQ+
Sbjct: 301  RDGRGIEITGSMGPGSGVLKDDYTNFGRLSLVKNDGKDILISGSNLSAIGMGTRDMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
            S+SLRESKG I    ADAMGFN+YKGGGK V T     ++++M
Sbjct: 361  SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FGTLASYMGSDGSGMSAGSGYSVNS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
            KN+                     T                QFAA    TA+    D+ AGV
Sbjct: 419  GKNMSALYEGNLAFV-------TAFSVAFGFSAKGDGTSQFAAFAGTASIAAKDQQAGV 470

Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
            TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 471  TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530
```

```
Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
               A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 531 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 566
```

```
tr   Q6L5K4      Flagellin (Fragment) [flaA] [Campylobacter lari]  567 AA
                                                                   align
```

```
 Score =  751 bits (1940), Expect = 0.0
 Identities = 404/576 (70%), Positives = 462/576 (80%), Gaps = 10/576 (1%)
```

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
               GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
```

```
Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
               GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120
```

```
Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
               ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT+++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180
```

```
Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
               +SGV LTIKNYNGI+DFKF VVIS+SVGTG+GALAEEIN+ AD TGVRA + V+TTG
Sbjct: 181 SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVQTTGA 240
```

```
Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
               +IK   TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300
```

```
Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
               DGRGI+ITG++ VGSG+L +  +N+GRLSLVKNDG+DI ISG+ LS IGMG  DMISQ+
Sbjct: 301 RDGRGIEITGNMEVGSGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360
```

```
Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
               S+SLRESKG I   ADAMGFN+YKGGGK V T   SSI AFM
Sbjct: 361 SISLRESKGNIDTHIADAMGFNAYKGGGKMVVT--FSSIEAFMSSDGSGMSAGSGFSIGS 418
```

```
Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
               K +              T                QFAA  TA+    D+ AGV
Sbjct: 419 GKEMSKIYNSGNLALV-------TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV 471
```

```
Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVQVNVKAAESQIRDVDF 539
               TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531
```

```
Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
               A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 567
```

```
tr   Q6L5K7      Flagellin (Fragment) [flaA] [Campylobacter lari]  563 AA
                                                                   align
```

tr   Q6L5J6   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 566 AA
                                                                    align

Score = 749 bits (1935), Expect = 0.0
Identities = 400/576 (69%), Positives = 464/576 (80%), Gaps = 11/576 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
             GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
             GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121   ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
             ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121   ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181   TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             +SGV LTIKNYNGI+DFKF VVIS+SVGTG+GALAEEIN+ +D TGVRA++ V+TTG
Sbjct: 181   SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVSDITGVRASFLVQTTGA 240

Query: 241   YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             +IK   TSQDF INGV IG++EYKDGD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241   GSIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301   ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
             DGRGI+ITG +G GSG+L +   N+GRLSLVKNDG+DI ISG+ LSAIGMGT DMISQ+
Sbjct: 301   RDGRGIEITGSMGPGSGVLKDDYTNFGRLSLVKNDGKDILISGSGLSAIGMGTADMISQA 360

Query: 361   SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
             S+SLRESKG I   ADAMGFN+YKGGGK V T   ++++M
Sbjct: 361   SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FGTLASYMGSDGSGMSAGSGYSVGS 418

Query: 421   XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
             K +   T   QFAA TA+   D+ AGV
Sbjct: 419   GKEMSALYEGNLAFV-------TAFSVAFGFSAKGDGTSQFAAFAGTASIAAKDQQAGV 470

Query: 480   TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
             TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 471   TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530

Query: 540   ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
             A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 531   AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 566

tr   Q6L5L1   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 566 AA
                                                                    align

Score = 747 bits (1929), Expect = 0.0
Identities = 399/576 (69%), Positives = 463/576 (80%), Gaps = 11/576 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
             GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL

```
Sbjct: 1    GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121  ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SGV LTIKNYNGI+DFKF VVIS+SVGTG+GALAEEIN+ +D TGVRA++ V+TTG
Sbjct: 181  SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVSDITGVRASFLVQTTGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             +IK   TSQDF INGV IG++EYKDGD NG+ ISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241  GSIKADKTSQDFTINGVRIGEVEYKDGDENGASISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
             DGRGI+ITG +G GSG+L +   N+GRLSLVKNDG+DI ISG+ LSAIGMGT DMISQ+
Sbjct: 301  RDGRGIEITGSMGPGSGVLKDDYTNFGRLSLVKNDGKDILISGSGLSAIGMGTADMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            S+SLRESKG  I    ADAMGFN+YKGGGK V T    ++++M
Sbjct: 361  SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FGTLASYMGSDGSGMSAGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
             K +                   T             QFAA   TA+    D+ AGV
Sbjct: 419  GKEMSALYEGNLAFV--------TAFSVAFGFSAKGDGTSQFAAFAGTASIAAKDQQAGV 470

Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
            TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 471  TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530

Query: 540  ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 531  AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 566
```

tr <u>O85181</u>   **Flagellin B [flaB] [Campylobacter jejuni]**   575 AA
                                                                       <u>align</u>

```
 Score = 747 bits (1928), Expect = 0.0
 Identities = 405/578 (70%), Positives = 451/578 (77%), Gaps = 7/578 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2    GFRINTNIGALNAHANSVVNARELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181
```

```
Query:  181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             +SG V   T+KNYNGI+DF+F   VVISTSVGTGLGALAEEINKSAD+TGVRAT+ V+T G+
Sbjct:  182  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALAEEINKSADQTGVRATFTVETRGM 241


Query:  241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A++ GTTS  FAINGV IG++ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct:  242  AAVRAGTTSDTFAINGVKIGQVAYEDGDANGALVSAINSVKDTTGVEASIDANGQLLLTS 301


Query:  301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
             +GRGIKI G IG G+ I  +  ENYGRLSLVKNDG+DI ISGT LS  G G ++ ISQ
Sbjct:  302  REGRGIKIEGSIGGGAFINKDMMENYGRLSLVKNDGKDILISGTGLSFTGFGASNFISQV 361


Query:  361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
             SVSLRESKG+  A  ADAMGF S   G        SSI+ +M
Sbjct:  362  SVSLRESKGRFDANTADAMGFGSVNKG----LVLAASSIADYMSAEGSGFSAGSGYSVGS 417


Query:  421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
              K               Y V                QFA +KT+A N+     DETA
Sbjct:  418  GKGYSATLTANAIAISSASAISKIYNVSQGSGFSSGSTLSQFATMKTSAGNSLGAKDETA 477


Query:  478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
             GVTTLKGAMAVMDIAETA TNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDV
Sbjct:  478  GVTTLKGAMAVMDIAETATTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDV 537


Query:  538  DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
             DFA+ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct:  538  DFAAESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 575
```

tr   Q6L5K0   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 565 AA
                                                                        align

```
 Score =  746 bits (1926), Expect = 0.0
 Identities = 400/576 (69%), Positives = 461/576 (79%), Gaps = 12/576 (2%)

Query:  1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
             GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct:  1    GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60


Query:  61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
             GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct:  61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120


Query:  121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
             ELDNIANTTSFNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ +
Sbjct:  121  ELDNIANTTSFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMAK 180


Query:  181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
              SGV   LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEIN+ AD TGVRA + V+TTG
Sbjct:  181  ESGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADITGVRANFLVQTTGA 240


Query:  241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             +IK   TSQDF INGV IG++EYK+GD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct:  241  GSIKADKTSQDFTINGVKIGEVEYKEGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300
```

```
Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            DGRGI+ITG+IGVGSGI+ +   +N+GRLSLVKNDG+DI ISG+ LS IGMG  DMISQ+
Sbjct: 301 RDGRGIEITGNIGVGSGIMKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAADMISQA 360


Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            S+SLRESKG I    ADAMGFN+YKGGGK + T   ++I  FM
Sbjct: 361 SISLRESKGNIDTHVADAMGFNAYKGGGKMIVTN--ANIGDFMSTNGMSAGTGYSVGSGK 418


Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAA-LKTTAANTTDETAGV 479
            +                       + V               QFAA L T +   D+ AGV
Sbjct: 419 DMS--------KVYEGNLAFVTAFSVAFGFSVGNGDGATQFAAFLNTASIAAKDQQAGV 469


Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
            TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 470 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 529


Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 530 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 565
```

tr   Q6L5K3   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   567 AA
                                                                      align


```
Score =  742 bits (1916), Expect = 0.0
Identities = 398/576 (69%), Positives = 458/576 (79%), Gaps = 10/576 (1%)
```

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 60


Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120


Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT+FNGKQLLSGNFTNQEFQIGA SNQTVKA+IG TQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGNFTNQEFQIGAQSNQTVKASIGPTQSSKIGVTRFETGSMSH 180


Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +SGV  LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEIN+ AD TGVRA + V+TTGV
Sbjct: 181 SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVETTGV 240


Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            AIK G TS DF INGV IG+IEY+D D NG+L++AIN+VKD+TGV+AS+D NG+LVL S
Sbjct: 241 GAIKAGVTSDDFTINGVKIGRIEYQDSDQNGALVAAINSVKDSTGVEASRDANGRLVLNS 300


Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            DGRGI+ITGD+G G+G+L +   +N+GRLSLVKNDG+DI ISG+ LS IGMG  DMISQ+
Sbjct: 301 RDGRGIEITGDMGPGAGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360


Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
            SVSLRESKG+I    ADAMGFN+YKGGGK V T   SSI AFM
Sbjct: 361 SVSLRESKGRIDPQMADAMGFNAYKGGGKMVIT--FSSIEAFMSSNGSGMSAGSGFSIGS 418


Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
```

```
            K +                    T              QFAA    TA+    D+  GV
Sbjct: 419 GKEMSKIYNSGNLALV-------TVFSNAFGFSAKNDGSSQFAAFAGTASIAANDQAPGV 471

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
           TTLKGAMA+MDI ETA  NLD IRADIG++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472 TTLKGAMAMMDIVETATANLDAIRADIGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 567
```

```
tr    P96751        Flagellin (Fragment) [flaA] [Campylobacter sp]  626 AA
                                                                    align
```

```
 Score =  605 bits (1560), Expect = e-172
 Identities = 358/630 (56%), Positives = 418/630 (65%), Gaps = 60/630 (9%)

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
           FRINT+VAALNAKANSDLN+K+LD SL+RLSSGLRINSAADDASGMAIADSLR+QA+TLG
Sbjct: 1   FRINTHVAALNAKANSDLNSKALDQSLARLSSGLRINSAADDASGMAIADSLRTQASTLG 60

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
           QAI+NGNDA  ILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LMEE
Sbjct: 61  QAINNGNDAASILQTADKAMDEQLKILDTIKVKATQAAQDGQSAKTRNMLQADINRLMEE 120

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
           LDNIANTTSFNGKQLLSG F NQEFQIGA SNQT+KA+IGATQSSKIGVTRFETGA   +
Sbjct: 121 LDNIANTTSFNGKQLLSGGFINQEFQIGAQSNQTIKASIGATQSSKIGVTRFETGANVTS 180

Query: 182 SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVY 241
           S +  +TIKNYNGI+DFK  NVVISTSVGTGLGALAEEIN+ AD+TGVRA+++V+T G
Sbjct: 181 SSIASMTIKNYNGIDDFKIQNVVISTSVGTGLGALAEEINRVADRTGVRASFNVQTVGGA 240

Query: 242 AIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENG------- 294
           + +G+TS DF INGV IGKI+Y+ GD NGSL+S+INAVKDTTGV+A+ +ENG
Sbjct: 241 PVLKGSTSDDFTINGVKIGKIDYESGDANGSLVSSINAVKDTTGVEAALNENGQLVLTSR 300

Query: 295 ------------------------KLVLTSADGRGIKITGD-IGVGSGILANQ----- 322
                               +L L  DGR I I+G  G  + L +Q
Sbjct: 301 EGRGIKIEGDMGSGAGIAVNMRENYGRLSLVKNDGRDIAISGTGFGFDNEKLVSQNSVSL 360

Query: 323 KENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFN 382
           ++ G++S   D  N S  +++I +G T M  +  L +   +  + GF+
Sbjct: 361 RDTKGQISQEIADAMGFN-SSNKVASIRIGVTAMSVLAGTGLSKETSLLYTAGS---GFS 416

Query: 383 SYKGGGKFVFTQNVSSI------SAFMXXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXX 436
           ++   K    I     SAF                     L
Sbjct: 417 AFTISAKSQLNMVGQVIDLGPKHSAFSGGYTALGFTAGSGFSAINSALSMLMYSKMYGTQ 476

Query: 437 XXXXXXNTYVVXXXXXXXXXXXXXXXXQFA-------ALKTTAANTT----DETAGVTTLKGA 485
                + V                  LK+  T    ++TAGVTTLKGA
Sbjct: 477 TGAAKFSVAVAMSTADIKFVSTISTGGLSGLYNDGLKSGETRTENIGQEQTAGVTTLKGA 536

Query: 486 MAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESAN 545
           MAVMD+AETAITNLD IRAD+GSIQNQ+++TINNITVTQVNVK+AES IRDVDFASESAN
```

```
Sbjct: 537  MAVMDVAETAITNLDTIRADLGSIQNQISATINNITVTQVNVKSAESTIRDVDFASESAN 596

Query: 546  YSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            YSKANILAQSGSYAMAQAN+SQQNVLRLLQ
Sbjct: 597  YSKANILAQSGSYAMAQANASQQNVLRLLQ 626
```

```
tr    P96752      Flagellin [flaB] [Campylobacter sp]        630 AA
                                                             align
```

```
 Score =  598 bits (1541), Expect = e-169
 Identities = 358/630 (56%), Positives = 411/630 (64%), Gaps = 56/630 (8%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN+ ALNA ANS +NA +LD SL+RLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2    GFRINTNIGALNAHANSVVNANALDKSLNRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 62   GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNGKQLLSG F NQEFQIGA SNQT+KA+IGATQSSKIGVTRFETGA
Sbjct: 122  ELDNIANTTSFNGKQLLSGGFINQEFQIGAQSNQTIKASIGATQSSKIGVTRFETGANVV 181

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
              SG+  LTIKNYNG+EDFKF ++VISTSVGTGLGALAEEIN+ ADKTGVRA+++V+TTG
Sbjct: 182  QSGIASLTIKNYNGLEDFKFRDIVISTSVGTGLGALAEEINRVADKTGVRASFNVQTTGG 241

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLV--- 297
             I  G T +DF+INGV IGKIEY+ GD NG+L+S+INAVKDTTGV+A+ DENG LV
Sbjct: 242  APIIAGVTGEDFSINGVIIGKIEYQAGDANGALVSSINAVKDTTGVEAALDENGHLVLTS 301

Query: 298  --------------------------LTSADGRGIKITGD-IGVGSGILANQ---- 322
                                      L   DGR I I+G   G  + L +Q
Sbjct: 302  REGRGIKIEGDMGSGAGIAVNMRENYGRLSLVKNDGRDIAISGTGFGFDNEKLVSQNSVS 361

Query: 323  -KENYGRLSLVKNDGRDINISGTNLSAIGMGTTDM-------ISQSSVSLRESKGQISAT 374
             ++ G++S    D   N S  +++I +G T M         +S+ +  L +    SA
Sbjct: 362  LRDTKGQISQEIADAMGFN-SSNKVASIRIGVTAMSVLAGTGLSKETSLLYTAGSGFSAF 420

Query: 375  NADAMGFNSYKG-----GGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
             A   +  G     G K     +  F                         K
Sbjct: 421  TISAKSQLNMVGQVIDLGPKHSAFSGGYTALGFTAGSGFSAINSALSMLMYSKMYGTQTG 480

Query: 430  XXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAAL----KTTAANTTDETAGVTTLKGA 485
                          N +                 Q L    K        ++TAGVTTLKGA
Sbjct: 481  AAKFSVAIAMSTTNIQINSAVSGTNGISGLYQTLGLEFGEKRIENIGQEQTAGVTTLKGA 540

Query: 486  MAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESAN 545
            MAVMDIAETA NLDQIRADIGS+QNQ+  TINNITVTQVNVKAAES IRDVDFA+ESAN
Sbjct: 541  MAVMDIAETATINLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFAAESAN 600

Query: 546  YSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            +SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 601  FSKYNILAQSGSYAMSQANAVQQNVLKLLQ 630
```

```
tr   Q84IC4      Flagellin (Fragment) [flaA] [Campylobacter lari]  491 AA
                                                                    align


 Score =  537 bits (1383), Expect = e-151
 Identities = 318/575 (55%), Positives = 381/575 (65%), Gaps = 84/575 (14%)


Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ LN+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1    GFRINTNGASLNAQVNAGLNSRNLDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60


Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120


Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT++NGKQLLSG+F+N +FQIG  +NQTV ATIG+T SSKIG TRFETGA
Sbjct: 121  ELDNIANTTTYNGKQLLSGSFSNAQFQIGDKANQTVNATIGSTNSSKIGQTRFETGAVIT 180


Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
               +   G TIK+Y+GI D+K D+V IS SVGTGLGALA EINK++DKTGVRAT  V+T
Sbjct: 181  AAVSNGFTIKSYDGINDYKIDSVAISYSVGTGLGALAAEINKASDKTGVRATATVQTISS 240


Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             + G+T   FAINGV +GK+ Y+ GD NG+L+SAINA KDTTGV+AS  + GKLVL S
Sbjct: 241  GTLTAGSTGASFAINGVVMGKVVYEAGDKNGALVSAINAKKDTTGVEASIVD-GKLVLNS 299


Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMTTDMISQS 360
            A                                DGR I +SG+      +GT    S
Sbjct: 300  A--------------------------------DGRGIKLSGS------IGT----SLE 316


Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
              L E+ G++S    D       G  F+   NVS+I
Sbjct: 317  GQMLEENYGRLSLVKND-------GSDIFISGTNVSNIGLGTAQMAEATVNLESVKGQI 368


Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             ++                                         F A+ T      ++AGVT
Sbjct: 369  TADIASAMG------------------------------FNAMSTADTAGKKQSAGVT 396


Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            +L+GAMAVMDIA+TAI NLD IRA+IG+ QNQ+TSTINNI+VTQVNVKAAESQIRDVDFA
Sbjct: 397  SLQGAMAVMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQIRDVDFA 456


Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSYAMAQAN++ QNVLRLLQ
Sbjct: 457  SESANYSKANILAQSGSYAMAQANAASQNVLRLLQ 491




tr   Q84IC5      Flagellin (Fragment) [flaA] [Campylobacter lari]  490 AA
                                                                    align


 Score =  534 bits (1375), Expect = e-150
 Identities = 313/575 (54%), Positives = 379/575 (65%), Gaps = 85/575 (14%)
```

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ LN+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1    GFRINTNGASLNAQVNAGLNSRNLDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT++NGKQLLSG+F+N +FQIG  +NQTV ATIG+T S+K+G TRFETGA
Sbjct: 121  ELDNIANTTTYNGKQLLSGSFSNAQFQIGDKANQTVNATIGSTNSAKVGQTRFETGAVIT 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            +   G TIK+Y+GI D+K D+V IS SVGTGLGALA EINK++DKTGVRAT  V+T
Sbjct: 181  AAVSNGFTIKSYDGINDYKIDSVAISYSVGTGLGALAAEINKASDKTGVRATATVQTISS 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            ++ G+T Q FAINGV IGK+ Y+ GD NG+L+SAINA KDTTGV+AS   +
Sbjct: 241  GSLAAGSTGQTFAINGVVIGKVVYEAGDKNGALVSAINAKKDTTGVEASIVD-------- 292

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
                                        G+L L   DGR I +SG+ + A+G
Sbjct: 293  -----------------------GKLVLNSADGRGIKLSGS-IGALG----------- 315

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
               L E+ G++S    D       G    F+     VS+I
Sbjct: 316  DQMLEENYGRLSLVKND-------GSNIFISGTTVSNIGLGTAQMAEATVNLESIKGQI 367

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             ++                                       F A+ T      ++AGVT
Sbjct: 368  TADIASAMG--------------------------------FNAMSTADTAGKKQSAGVT 395

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
            TL+GAMAVMDIA+TAI NLD IRA+IG+ QNQ+TSTINNI+VTQVNVKAAESQIRDVDFA
Sbjct: 396  TLQGAMAVMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQIRDVDFA 455

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            SESANYSKANILAQSGSYAMAQAN++ QNVLRLLQ
Sbjct: 456  SESANYSKANILAQSGSYAMAQANAASQNVLRLLQ 490
```

tr   Q84IC7   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   491 AA
                                                                        align

Score = 523 bits (1346), Expect = e-147
Identities = 316/575 (54%), Positives = 374/575 (64%), Gaps = 84/575 (14%)

```
Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ LN+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL
Sbjct: 1    GFRINTNGASLNAQVNAGLNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
```

```
              ELDNIANTTS+NGKQLLSG+F+N +FQIG  +NQTV ATIGAT S KIG TRFETGA+
Sbjct: 121 ELDNIANTTSYNGKQLLSGSFSNAQFQIGDKANQTVNATIGATNSGKIGQTRFETGARIT 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
              SG  GLTIK+Y+G+ DF   V ISTS GTGLGALA EINKS+D TGVRAT  V+T
Sbjct: 181 ASGSSGLTIKSYDGVNDFVIQPVTISTSAGTGLGALAAEINKSSDITGVRATATVQTISS 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
              +IK GTT ++F+INGV IGK+  +D D +G+L+SA        + A KD  G
Sbjct: 241 GSIKAGTTGENFSINGVIIGKVSVQDNDKDGALVSA---------INAKKDTTGV----- 286

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
                          + N    G+L L   DGR I + G+     +GT   S S
Sbjct: 287 --------------EASMVN-----GQLVLNSADGRGIELGGS------LGT----SLS 316

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
               V   + G++S    D G +    GG +   + S +A
Sbjct: 317 GVVASVNYGRLSLVKND--GSDIIVNGGSLIGLGSAGSKAA----------------EA 357

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
             NL                                       F A+ T A    +TAGVT
Sbjct: 358 TVNLESIKGEISADVASAMG--------------------FNAMTTAALAGKKQTAGVT 396

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
              TL+GAMAVMDIA+TAI NLD IRA+IG+ QNQ+TSTINNI+VTQVNVKAAESQIRDVDFA
Sbjct: 397 TLQGAMAVMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQIRDVDFA 456

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
              SESANYSKANILAQSGSYAMAQAN++ QNVLRLLQ
Sbjct: 457 SESANYSKANILAQSGSYAMAQANAASQNVLRLLQ 491
```

```
tr   Q84IC8      Flagellin (Fragment) [flaA] [Campylobacter lari]  492 AA
                                                                    align
```

Score = 481 bits (1239), Expect = e-134
Identities = 255/391 (65%), Positives = 314/391 (80%), Gaps = 4/391 (1%)

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
             GFRINTN A+LNA+ N+ LN+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1   GFRINTNGASLNAQVNAGLNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
             GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVRFETGAQSF 180
             ELDNIANTTS+NGKQLLSG+F NQ+FQIG  +NQTV ATIGAT S+KIG TRFETG++
Sbjct: 121 ELDNIANTTSYNGKQLLSGSFANQQFQIGDKANQTVNATIGATNSAKIGQTRFETGSKIS 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             +  +G TIK+Y+G+ D++   V +S S GTGLGALA EINKS+D TGVRAT  V+T
Sbjct: 181 AATNIGFTIKSYDGVNDYQIQAVAVSYSAGTGLGALAAEINKSSDITGVRATATVQTISS 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
              IK GTT +DF+INGV IGK+E KDGD +G+L+SAINA KDTTGV+AS  NG+LVL S
```

```
Sbjct: 241 GTIKTGTTGEDFSINGVIIGKVEVKDGDKDGALVSAINAKKDTTGVEASM-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVG-SGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQ 359
           ADGRGI + G +G   SG++A+   N+GRLSLVKNDG DI ISGTN S +G+G++    ++
Sbjct: 300 ADGRGIVLGGSLGTSLSGVVAS--ANFGRLSLVKNDGSDIIISGTNASQLGIGSSATTAE 357

Query: 360 SSVSLRESKGQISATNADAMGFNSYKGGGKF 390
           ++V+L   KG+ISA  A AMGFN+       F
Sbjct: 358 ATVNLESIKGEISADIASAMGFNAMSTAATF 388




tr   Q93GT4        Flagellin (Fragment) [flaA] [Campylobacter lari]  486 AA
                                                                      align

 Score =  476 bits (1225), Expect = e-133
 Identities = 258/384 (67%), Positives = 310/384 (80%), Gaps = 9/384 (2%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASGMAIADSLR+QA +L
Sbjct: 1   GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGMAIADSLRNQAASL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61  GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTT++NGKQLLSG F+NQ+FQIG +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121 ELDNIANTTTYNGKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            SG  G TIKNY+G+ DFK  +V++STS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 181 GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAAEINKSSDKTGVRATATVQTISS 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           I+ G T  F INGV IGK+  + GD +GSL++AINA KDTTGV+AS   NG+LVL S
Sbjct: 241 GTIQAGNTGDTFTINGVVIGKVAVQAGDKDGSLVAAINAKKDTTGVEASV-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVGSGILAN-QKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQ 359
           ADGRGI+++  G+G+ +  N    NYGRLSLVKNDG DI ISG  S  G GT   +++
Sbjct: 300 ADGRGIELS---GLGTALSGNIASVNYGRLSLVKNDGSDIIISGG--SGAGFGTA--VAE 352

Query: 360 SSVSLRESKGQISATNADAMGFNS 383
           ++V+L   KGQISA  A AMGFN+
Sbjct: 353 ATVNLESVKGQISADIACAMGFNA 376




tr   Q8RTY4        Flagellin (Fragment) [flaA] [Campylobacter lari]  491 AA
                                                                      align

 Score =  475 bits (1222), Expect = e-132
 Identities = 250/383 (65%), Positives = 309/383 (80%), Gaps = 3/383 (0%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL
Sbjct: 1   GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60
```

```
Query:  61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct:  61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT++NGKQLLSG+F+NQ+FQIG  +NQTV ATIG+T SSKIG TRFETGA+
Sbjct: 121  ELDNIANTTTYNGKQLLSGSFSNQQFQIGDKANQTVNATIGSTNSSKIGQTRFETGARVT 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             G + +T+KNY+GI D+KF NV IST VGTGLGALA EINK++DKTGVRA+  V+T
Sbjct: 181  GGGDISITLKNYDGINDYKFQNVTISTGVGTGLGALAAEINKASDKTGVRASATVQTIST 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A+  G+T + F INGV IGK+ +K+GD +G+L+SAINA KDTTGV+AS   +GKLVL S
Sbjct: 241  AALTAGSTGEGFTINGVVIGKVVFKEGDKDGALVSAINAKKDTTGVEAS-IVDGKLVLNS 299

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIK++G +G      +A  +ENYGRL+LVKNDG DI +S T       T  +S++
Sbjct: 300  ADGRGIKLSGTLGALDTQIA--EENYGRLTLVKNDGSDIVVSTTGAGFSTGATNAGLSEA 357

Query: 361  SVSLRESKGQISATNADAMGFNS 383
            +V+L   KG+ISA  A AMGFN+
Sbjct: 358  TVNLESIKGEISADIASAMGFNA 380
```

tr   Q56746   **Flagellin [flag] [Wolinella succinogenes]**   518 AA
                                                                    align

```
 Score =  474 bits (1221), Expect = e-132
 Identities = 288/588 (48%), Positives = 363/588 (60%), Gaps = 86/588 (14%)

Query:  2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
            F+INTNV+ALNA+A    N+  L +SL +LSSGLRIN AADDASGMAIADSLR+QAN+LG
Sbjct:  3   FQINTNVSALNAQAQGGFNSTKLSSSLEKLSSGLRINKAADDASGMAIADSLRTQANSLG 62

Query: 62   QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QAI N ND +GI+Q ADKAMDEQ+KILDTIKTKATQ+AQDGQ+  TR  LQADIN+L+E
Sbjct: 63   QAIKNTNDGIGIVQIADKAMDEQIKILDTIKTKATQSAQDGQTTTTRKALQADINRLIEG 122

Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
            LDNIA TTS+NG+ LLSG+FTN+EFQ+GA SNQT+KA+IGAT S KIG  R ET  Q
Sbjct: 123  LDNIAATTSYNGQSLLSGSFTNKEFQVGAYSNQTIKASIGATSSDKIGQVRLETSGQIVA 182

Query: 182  SG------VVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDV 235
            S        V L   N +G   + ++V ISTS GTG+G L E INK++D  V+A++ V
Sbjct: 183  SAGGSSLTSVALKFVNVDGTNSVQLESVKISTSAGTGIGVLVETINKNSDALNVKASWSV 242

Query: 236  KTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQASKDENG 294
            + TG  + GT  +   ING+TIG + + +  D +G LI+AINAVKD TGV+AS DE G
Sbjct: 243  QATGSTNVASGTI-KGLEINGITIGTVTDVQKNDSDGRLIAAINAVKDQTGVEASIDEQG 301

Query: 295  KLVLTSADGRGIKI---TGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGM 351
            +L L S DGR +++   +    +G G +               GT   + G
Sbjct: 302  RLNLNSTDGRAVQVKTTSASTILGGGSM--------------------GTASAGAGA 338
```

```
Query: 352 GTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXX 411
                T  I+ + + R+   QIS TNA+ +G  +  GG         S I A
Sbjct: 339 TTVGRITLTRLDARDI--QISGTNANLVGLVASGGGAG-------SGIGAM--------- 380


Query: 412 XXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAAN 471
                                               T V                 A     A+
Sbjct: 381 -----------------------------AETTVNLRDVKGKFNENVASAAGANANASI 410


Query: 472 TTDET----AGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNV 527
              TD      AGVT+LKGAM VMDIAE+AI   LD++R+D+GS+QNQ+TST+NNIT+TQVNV
Sbjct: 411 ATDNANGIGAGVTSLKGAMVVMDIAESAIKMLDKVRSDLGSVQNQMTSTVNNITITQVNV 470


Query: 528 KAAESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
             +AAES IR+VDFA+ES+NYSK NILAQ+GSYAM+QANSSQQN+LRLLQ
Sbjct: 471 QAAESNIREVDFAAESSNYSKLNILAQAGSYAMSQANSSQQNILRLLQ 518
```

tr   Q93R24   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   486 AA
                                                                        align

 Score = 474 bits (1220), Expect = e-132
 Identities = 257/384 (66%), Positives = 309/384 (79%), Gaps = 9/384 (2%)

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASGMAIADSLR+QA +L
Sbjct: 1   GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGMAIADSLRNQAASL 60


Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61  GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120


Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTT++NGKQLLSG F+NQ+FQ+G  +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121 ELDNIANTTTYNGKQLLSGAFSNQQFQVGDKANQTINATIGATQSAKIGQTRFETGSRIT 180


Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             SG  G TIKNY+G+ DFK  +V++STS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 181 GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAAEINKSSDKTGVRATATVQTISS 240


Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           I+  G T   F INGV IGK+ + GD +GSL++AINA KDTTGV+AS   NG+LVL S
Sbjct: 241 GTIQAGNTGDTFTINGVVIGKVAVQAGDKDGSLVAAINAKKDTTGVEASV-VNGQLVLNS 299


Query: 301 ADGRGIKITGDIGVGSGILAN-QKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQ 359
           ADGRGI+++  G+G+ + N    NYGRLSLVKNDG DI ISG  S G GT    ++
Sbjct: 300 ADGRGIELS---GLGTALSGNIASVNYGRLSLVKNDGSDIIISGG--SGAGFGTA--AAE 352


Query: 360 SSVSLRESKGQISATNADAMGFNS 383
           ++V+L   KGQISA  A AMGFN+
Sbjct: 353 ATVNLESVKGQISADIACAMGFNA 376
```

tr   Q7M7N1   **FLAGELLIN B [FLAB] [Wolinella succinogenes]**   513 AA
                                                                      align

```
Score =  473 bits (1217), Expect = e-132
Identities = 292/586 (49%), Positives = 365/586 (61%), Gaps = 85/586 (14%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            G+RINTNVAALNA A     N +SL++SL +LSSGLR+N AADDASGMAIADSLRSQA +L
Sbjct: 2    GYRINTNVAALNAHAIGVQNNRSLNSSLEKLSSGLRVNKAADDASGMAIADSLRSQAASL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQA N NDA+GI+QTADKAMDEQ+KILDTIKTKA QAAQDGQ+ +TR LQ+DI +L+E
Sbjct: 62   GQATRNANDAIGIIQTADKAMDEQIKILDTIKTKAVQAAQDGQTTETRKALQSDILRLLE 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTTSFNG+++LSG+F N+EFQIGA SN T+KA+IGAT S+KIG  R ET + S
Sbjct: 122  ELDNIANTTSFNGQEMLSGSFVNKEFQIGAYSNTTIKASIGATSSNKIGHVRLETSSISA 181

Query: 181  TSGV----------VGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVR 230
            +S +           V  +  +G  F+ + V ISTS GTG+GALAE INK+++  GVR
Sbjct: 182  SSMLASAGGSNLTEVAFKVLQVDGKNSFQLETVKISTSAGTGIGALAEVINKNSNVLGVR 241

Query: 231  ATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQAS 289
            A+Y+V TG   I+ GT +    INGVTIG I + +  D +G LI+AINAVK+ TGV+A
Sbjct: 242  ASYEVMGTGSLPIQSGTVNT-LVINGVTIGTINDIQKNDADGKLINAINAVKEATGVEAY 300

Query: 290  KDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAI 349
            D +G+L L S DGR I ++   G G                V  G I  SG++ + +
Sbjct: 301  TDISGRLTLKSTDGRAISVSTVSGAG---------------VLGGGSFIGTSGSSHAIV 344

Query: 350  GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXX 409
            G T  ++  V      IS TN  +GF+S +  G  +T N+  +    M
Sbjct: 345  GRLTLTRLNARDVL-------ISGTNFSHVGFHSAQ--GIAEYTVNLRDLRGEMNANIAS 395

Query: 410  XXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTA 469
                                                                    A L   +
Sbjct: 396  AAGAN--------------------------------------------------ANLAIAS 407

Query: 470  ANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKA 529
            AN     AGVT+L GAM VMD+AE+A   LD+IRAD+GS+Q Q+TSTINNITVTQVNV A
Sbjct: 408  ANANGIGAGVTSLAGAMIVMDMAESARIQLDKIRADLGSVQAQLTSTINNITVTQVNVAA 467

Query: 530  AESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            AES+IRDVDFA ESA +SK NILAQSGS+AMAQAN+ QQNVL+LLQ
Sbjct: 468  AESEIRDVDFAEESATFSKHNILAQSGSFAMAQANTVQQNVLKLLQ 513
```

```
tr   Q84IC9      Flagellin (Fragment) [flaA] [Campylobacter lari]  500 AA
                                                                     align
```

```
Score =  471 bits (1213), Expect = e-131
Identities = 257/390 (65%), Positives = 307/390 (77%), Gaps = 8/390 (2%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIAD+L++QANTL
Sbjct: 1    GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADNLKTQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +I KLME
```

```
Sbjct:  61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEITKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQ-S 179
            ELDNIANTT++NGKQLLSG+F NQ+FQIG  +NQT+ ATIGAT S+KIG +RFETG   +
Sbjct: 121  ELDNIANTTTYNGKQLLSGSFANQKFQIGDKANQTINATIGATYSAKIGQSRFETGQTIT 180

Query: 180  FTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTG 239
             ++G  +TIKNY+GI D+KF  V ISTS GTGLGALA EINK++D TGVRAT  V+T
Sbjct: 181  ASTGTASITIKNYDGINDYKFQAVTISTSAGTGLGALAAEINKASDITGVRATAIVQTVS 240

Query: 240  VYAI-KEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVL 298
            AI   GTT  DFAINGV IGK+ YK  D G+L+SAINA KDTTGV+AS   +GKLVL
Sbjct: 241  SGAIGASGTTGDDFAINGVVIGKVNYKANDKEGALVSAINAKKDTTGVEAS-IVDGKLVL 299

Query: 299  TSADGRGIKITGDIGVG----SGILAN-QKENYGRLSLVKNDGRDINISGTNLSAIGMGT 353
            S DGRGI ITG +G G        AN +ENYGRLSLVKNDG DI ISGT S +G+G+
Sbjct: 300  NSIDGRGINITGSVGSGLSGDGAAAANLLRENYGRLSLVKNDGSDIIISGTTASLLGVGS 359

Query: 354  TDMISQSSVSLRESKGQISATNADAMGFNS 383
                ++++V+L   KGQISA  A AMGFN+
Sbjct: 360  GGTTAEATVNLESVKGQISADMASAMGFNA 389
```

tr   Q93GT1   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 491 AA
                                                                         align

```
Score =  469 bits (1207), Expect = e-131
Identities = 247/383 (64%), Positives = 308/383 (79%), Gaps = 3/383 (0%)

Query:   1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL
Sbjct:   1  GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60

Query:  61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct:  61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT++NGKQLLSG+F+NQ+FQIG  +NQTV ATIG+T S+KIG TRFETGA+
Sbjct: 121  ELDNIANTTTYNGKQLLSGSFSNQQFQIGDKANQTVNATIGSTNSAKIGQTRFETGARVT 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
            + G + +T+KNY+GI D+KF +V +ST VGTGLGALA EINK +D+TGVRA+  V+T
Sbjct: 181  SGGDIAITLKNYDGINDYKFQSVTVSTGVGTGLGALAAEINKVSDQTGVRASATVQTIST 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             A+  G+T + F INGV IGK+ +K GD G+L+SAINA KDTTGV+AS   +GKLVL S
Sbjct: 241  AALTAGSTGEGFTINGVVIGKVVFKAGDKDGALVSAINAKKDTTGVEAS-IVDGKLVLNS 299

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGIK++G IG      +A +ENYGRL+LVKNDG DI +S T     T     +S++
Sbjct: 300  ADGRGIKLSGSIGDLDAQIA--EENYGRLTLVKNDGSDIVVSTTGAGFSTGATNAGLSEA 357

Query: 361  SVSLRESKGQISATNADAMGFNS 383
            +V+L   KG+ISA  A AMGFN+
Sbjct: 358  TVNLESIKGEISADIASAMGFNA 380
```

```
tr    Q84IC3        Flagellin (Fragment) [flaA] [Campylobacter lari]  487 AA
                                                                      align

 Score =  469 bits (1206), Expect = e-131
 Identities = 253/384 (65%), Positives = 310/384 (79%), Gaps = 9/384 (2%)

Query:   1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL  60
             GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct:   1   GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL  60

Query:  61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME  120
             GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct:  61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME  120

Query: 121   ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF  180
             ELDNIANTT++NGKQLLSG F+NQ+FQIG  +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121   ELDNIANTTTYNGKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT  180

Query: 181   TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV  240
              SG  G TIKNY+G+ DFK +V++STS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 181   GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAAEINKSSDKTGVRATATVQTISS  240

Query: 241   YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS  300
              I+ G T  F INGV IGK+ + GD +GSL++AINA KDTTGV+AS   NG+LVL S
Sbjct: 241   GTIQAGNTGDTFTINGVVIGKVAVQAGDKDGSLVAAINAKKDTTGVEASV-VNGQLVLNS  299

Query: 301   ADGRGIKITGDIGVGSGILAN-QKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQ  359
             ADGRGI+++  G+G+ + N     NYGRLSLVKNDG DI ISG  SA+G+GT   ++
Sbjct: 300   ADGRGIELS---GLGTALSGNIASVNYGRLSLVKNDGSDIIISGG--SAVGLGTA--TAE  352

Query: 360   SSVSLRESKGQISATNADAMGFNS  383
             ++V+L   KGQI+A+ A AMGFN+
Sbjct: 353   ATVNLESVKGQIAASIACAMGFNA  376
```

```
tr    Q84IC6        Flagellin (Fragment) [flaA] [Campylobacter lari]  487 AA
                                                                      align

 Score =  468 bits (1205), Expect = e-130
 Identities = 253/384 (65%), Positives = 310/384 (79%), Gaps = 9/384 (2%)

Query:   1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL  60
             GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct:   1   GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL  60

Query:  61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME  120
             GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct:  61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME  120

Query: 121   ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF  180
             ELDNIANTT++NGKQLLSG F+NQ+FQIG  +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121   ELDNIANTTTYNGKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT  180
```

```
Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             SG  G TIKNY+G+ DFK  +V++STS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 181  GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAAEINKSSDKTGVRATATVQTISS 240


Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             I+ G T  F INGV IGK+  + GD +GSL++AINA KDTTGV+AS   NG+LVL S
Sbjct: 241  GTIQAGNTGDPFTINGVVIGKVAVQAGDKDGSLVAAINAKKDTTGVEASV-VNGQLVLNS 299


Query: 301  ADGRGIKITGDIGVGSGILAN-QKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQ 359
             ADGRGI+++  G+G+ + N   NYGRLSLVKNDG DI ISG  SA+G+GT    ++
Sbjct: 300  ADGRGIELS---GLGTALSGNIASVNYGRLSLVKNDGDDIIISGG--SAVGLGTA--TAE 352


Query: 360  SSVSLRESKGQISATNADAMGFNS 383
             ++V+L   KGQI+A+ A AMGFN+
Sbjct: 353  ATVNLESVKGQIAASIACAMGFNA 376
```

tr   Q84IC2   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   500 AA
                                                                       align

```
Score = 466 bits (1199), Expect = e-130
Identities = 257/391 (65%), Positives = 310/391 (78%), Gaps = 10/391 (2%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL
Sbjct: 1    GFRINTNGASLNAQVNAGINSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60


Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120


Query: 121  ELDNIANTTSFN-GKQLLSG-NFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQ 178
            ELDNIANTT++N GKQLLSG  F+NQ+FQIG  +NQT+ ATIGAT S+KIG +RFETG Q
Sbjct: 121  ELDNIANTTTYNTGKQLLSGAYFSNQQFQIGDKANQTINATIGATYSAKIGQSRFETG-Q 179


Query: 179  SFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTT 238
             T+   +TIKNY+GI DFK  +V +STS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 180  RITASRASITIKNYDGINDFKIQSVTLSTSAGTGLGALAAEINKSSDKTGVRATATVQTI 239


Query: 239  GVYAI-KEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLV 297
             AI   G T DF INGV IGK+ YK  D +G+L+SAINA KDTTGV+AS   +GKLV
Sbjct: 240  SSGAIGASGNTGDDFTINGVVIGKVAYKANDKDGALVSAINAKKDTTGVEAS-IVDGKLV 298


Query: 298  LTSADGRGIKITGDIGVG----SGILAN-QKENYGRLSLVKNDGRDINISGTNLSAIGMG 352
            L SADGRGI+++G +G G    S  +AN   ENYGRLSLVKNDG DI +SGT S +G+G
Sbjct: 299  LNSADGRGIELSGSLGSGLSGDSAAIANLLSENYGRLSLVKNDGSDIIVSGTTASLLGVG 358


Query: 353  TTDMISQSSVSLRESKGQISATNADAMGFNS 383
            +    ++++V+L   KGQI+A  A AMGFN+
Sbjct: 359  SGGATAEATVNLESVKGQIAADIASAMGFNA 389
```

tr   Q93GT2   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   487 AA
                                                                       align

```
Score =   462 bits (1190), Expect = e-129
Identities = 253/383 (66%), Positives = 306/383 (79%), Gaps = 7/383 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1    GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIA TT++NGKQLLSG F+NQ+FQIG  +NQTV ATIG+T SSKIG TRFETG++
Sbjct: 121  ELDNIATTTTYNGKQLLSGAFSNQQFQIGDKANQTVNATIGSTNSSKIGQTRFETGSRVT 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             G +G TIKNY+G+ DFK  VVISTS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 181  AGGNLGFTIKNYDGVNDFKVQPVVISTSAGTGLGALAAEINKSSDKTGVRATAVVQTISS 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             I+ G T  F INGV IGK+ + GD +GSL++AINA KDTTGV+AS   NG+LVL S
Sbjct: 241  GTIQAGNTGDTFTINGVVIGKVAVRAGDKDGSLVAAINAKKDTTGVEASV-VNGQLVLNS 299

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
            ADGRGI+I+G  SG +A+  NYGRLSLVKNDG DI ISG  S +G+GT   +++
Sbjct: 300  ADGRGIEISGLGSALSGHIAS--VNYGRLSLVKNDGSDIIISGG--STVGLGTA--TAEA 353

Query: 361  SVSLRESKGQISATNADAMGFNS 383
            +V+L   KGQI+A+ A AMGFN+
Sbjct: 354  TVNLESVKGQIAASIACAMGFNA 376
```

tr Q84IC1   **Flagellin (Fragment) [flaA] [Campylobacter lari]** 487 AA
                                                                   align

```
Score =   462 bits (1189), Expect = e-129
Identities = 253/383 (66%), Positives = 306/383 (79%), Gaps = 7/383 (1%)

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1    GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT++NGKQLLSG F+NQ+FQIG  +NQTV ATIG+T SSKIG TRFETG++
Sbjct: 121  ELDNIANTTTTYNGKQLLSGAFSNQQFQIGDKANQTVNATIGSTNSSKIGQTRFETGSRVT 180

Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             G +G TIKNY+G+ DFK  VVISTS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 181  AGGNLGFTIKNYDGVNDFKVQPVVISTSAGTGLGALAAEINKSSDKTGVRATAVVQTISS 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
             I+ G T    INGV IGK+ + GD +GSL++AINA KDTTGV+AS   NG+LVL S
```

```
Sbjct: 241 GTIQAGNTGDTLTINGVVIGKVAVQAGDKDGSLVAAINAKKDTTGVEASV-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           ADGRGI+I+G    SG +A+   NYGRLSLVKNDG DI ISG   S +G+GT    +++
Sbjct: 300 ADGRGIEISGLGSALSGHIAS--VNYGRLSLVKNDGSDIIISGG--STVGLGTA--TAEA 353

Query: 361 SVSLRESKGQISATNADAMGFNS 383
           +V+L   KGQI+A+ A AMGFN+
Sbjct: 354 TVNLESVKGQIAASIACAMGFNA 376
```

---

tr   <u>Q93GT3</u>   **Flagellin (Fragment) [flaA] [Campylobacter lari]**   492 AA
<div align="right"><u>align</u></div>

```
 Score =  456 bits (1173), Expect = e-127
 Identities = 249/390 (63%), Positives = 305/390 (77%), Gaps = 6/390 (1%)

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN A+LNA+ N+ LN+++LD SL+RLSSGLRINSAADDASG+AIAD+L++QANTL
Sbjct: 1   GFRINTNGASLNAQVNAGLNSRALDQSLNRLSSGLRINSAADDASGLAIADNLKTQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTT++NGKQLLSG+F+NQ+FQIG  +NQTV ATIG+T S+KIG TRFETGA+
Sbjct: 121 ELDNIANTTTYNGKQLLSGSFSNQQFQIGDKANQTVNATIGSTNSAKIGQTRFETGARVT 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
           S  V  +  Y+GI D++F +V +S SVGTGLGALA EINK AD+TGVRA+  V+T
Sbjct: 181 GSTDVAFKLLRYDGINDYQFQSVAVSYSVGTGLGALAAEINKVADQTGVRASATVQTISS 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           A+  G+T + FAINGV IGK++Y+ GD +G+L+SAINA KDTTGV+AS   +GKLVL S
Sbjct: 241 GALTAGSTGEGFAINGVVIGKVKYQAGDKDGALVSAINAKKDTTGVEAS-IVDGKLVLNS 299

Query: 301 ADGRGIKITGDIGVGSGILANQ--KENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMIS 358
           ADGRGIK++G IG  G L Q  +ENYGRL+LVKNDG DI IS T        T   +S
Sbjct: 300 ADGRGIKLSGTIG---GDLEAQMVEENYGRLTLVKNDGSDIIISTTAGGFSANATAAGLS 356

Query: 359 QSSVSLRESKGQISATNADAMGFNSYKGGG 388
           +++ +L   KG+ISA  A AMGFN+    G
Sbjct: 357 EATTNLESIKGEISADIASAMGFNAMSTAG 386
```

---

tr   <u>Q46462</u>   **Flagellin (Fragment) [fla2] [Campylobacter**   436 AA
                        upsaliensis] <u>align</u>

```
 Score =  451 bits (1160), Expect = e-125
 Identities = 234/306 (76%), Positives = 263/306 (85%), Gaps = 3/306 (0%)

Query: 78  DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLL 137
           DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTTSFNGKQLL
Sbjct: 1   DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTTSFNGKQLL 60
```

```
Query: 138  SGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIED 197
            SG F NQEFQIG+SSNQT+KATIGA+QSSKIG+TRFETG Q   SG   +TIKNYNGI+D
Sbjct: 61   SGGFINQEFQIGSSSNQTIKATIGASQSSKIGLTRFETGTQVIQSGTAQMTIKNYNGIDD 120

Query: 198  FKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGV 257
            FKF  V ISTSVGTGLGALAEEIN+ ADKTGVRA+++V+T G  +I +GTT+   FAINGV
Sbjct: 121  FKFQAVKISTSVGTGLGALAEEINRVADKTGVRASFNVQTVGARSIMKGTTNDAFAINGV 180

Query: 258  TIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSG 317
            TIGK+ Y++ D NG+LI+AINAVKDTTGVQA+ DE GKLVLTSADGRGIKITG IG G+G
Sbjct: 181  TIGKVAYENNDSNGALIAAINAVKDTTGVQAALDEEGKLVLTSADGRGIKITGSIGPGAG 240

Query: 318  ILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNAD 377
            I N +ENYGRLSLVKNDGRDI I GT   +G   ++SQSS+SLRE+KGQIS   A+
Sbjct: 241  IALNMQENYGRLSLVKNDGRDIAIEGT---GVGFDNDKLVSQSSISLRETKGQISKDLAE 297

Query: 378  AMGFNS 383
            AMGFNS
Sbjct: 298  AMGFNS 303
```

tr   <u>Q46461</u>   **Flagellin (Fragment) [fla1] [Campylobacter**   436 AA
                       upsaliensis]   <u>align</u>

 Score = 446 bits (1147), Expect = e-124
 Identities = 230/306 (75%), Positives = 261/306 (85%), Gaps = 3/306 (0%)

```
Query: 78   DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLL 137
            DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTTSFNGKQLL
Sbjct: 1    DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTTSFNGKQLL 60

Query: 138  SGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIED 197
            SG F NQEFQIG+ SNQT+KATIG TQS+KIG+TRFETGAQ   S V + IKNYNG+ED
Sbjct: 61   SGGFINQEFQIGSQSNQTIKATIGPTQSNKIGLTRFETGAQIIKSSEVEMVIKNYNGLED 120

Query: 198  FKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGV 257
            FKF  + ISTSVGTGLGALAEEIN+ ADKTGVRA+++V+T G   + +GTT+++FAINGV
Sbjct: 121  FKFPKIKISTSVGTGLGALAEEINRVADKTGVRASFNVQTVGARPVMKGTTNENFAINGV 180

Query: 258  TIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSG 317
            TIGK+ Y++ D NG+LI+AINAVKDTTGVQA+ DE GKLVLTSADGRGIKITG IG G+G
Sbjct: 181  TIGKVAYENNDSNGALIAAINAVKDTTGVQAALDEEGKLVLTSADGRGIKITGSIGPGAG 240

Query: 318  ILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNAD 377
            I N +ENYGRLSLVKNDGRDI I GT      G   ++SQSS+SLRE+KGQIS   A+
Sbjct: 241  IALNMQENYGRLSLVKNDGRDIAIEGT---GFGFDNDKLVSQSSISLRETKGQISKDLAE 297

Query: 378  AMGFNS 383
            AMGFNS
Sbjct: 298  AMGFNS 303
```

sp   <u>Q9XB38</u>   **Flagellin A [flaA] [Helicobacter felis]**   512 AA
      FLAA_HELFE   <u>align</u>

```
tr Q7X2D1  Flagellin A [flaA] [Helicobacter pylori (Campylobacter        510
           pylori)]                                                       AA
                                                                          align


 Score =  443 bits (1140), Expect = e-123
 Identities = 265/576 (46%), Positives = 346/576 (60%), Gaps = 72/576 (12%)

Query: 2    FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
            F++NTN+ A+NA   S L  +L  SL RLSSGLRIN AADDASGM +ADSLRSQAN+LG
Sbjct: 3    FQVNTNINAMNAHVQSALTQNALKTSLERLSSGLRINKAADDASGMTVADSLRSQANSLG 62

Query: 62   QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QAI+N ND +GI+Q ADKAMDEQLKILDT+K KATQAAQDGQ+ ++R  +Q+DI +L++
Sbjct: 63   QAIANTNDGMGIIQVADKAMDEQLKILDTVKVKATQAAQDGQTTESRKAIQSDIVRLIQG 122

Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
            LDNI NTT++NG+ LLSG FTN+EFQ+GA SNQ++KA+IG+T S KIG  R   TGA
Sbjct: 123  LDNIGNTTTYNGQALLSGQFTNKEFQVGAYSNQSIKASIGSTTSDKIGQVRIATGALITA 182

Query: 182  SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVY 241
            SG + LT K +G+ D  ++V IS+S GTG+G LAE INK++++TGV+A   V TT
Sbjct: 183  SGDISLTFKQVDGVNDVTLESVKISSSAGTGIGVLAEVINKNSNQTGVKAYASVITTSDV 242

Query: 242  AIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ G+ S +  +NG+ +G I + K D +G L++AINAV   TGV+A  D+NG
Sbjct: 243  AVQSGSLS-NLTLNGIHLGNIADIKKNDSDGRLVAAINAVTSETGVEAYTDQNG------ 295

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMIS-- 358
                            RL+L  DGR I I  ++S G     M++
Sbjct: 296  ------------------------RLNLRSLDGRGIEIKTDSVSN-GPSALTMVNGG 327

Query: 359  QSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXX 418
            Q      + G++S T DA              NV S S
Sbjct: 328  QDLTKGSTNYGRLSLTRLDAKSI-------------NVVSASDSQHLGFTAIGFGESQVA 374

Query: 419  XXXKNLXXXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
               NL                       V+                  A+        AG
Sbjct: 375  ETTVNLRDVTGNFNANVKSASGANYNAVI-------------------ASGNQSLGAG 413

Query: 479  VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
            VTTL+GAM V+DIAE+A+   LD++R+D+GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVD
Sbjct: 414  VTTLRGAMVVIDIAESAMKMLDKVRSDLGSVQNQMISTVNNISITQVNVKAAESQIRDVD 473

Query: 539  FASESANYSKANILAQSGSYAMAQANSSQQNVLRLL 574
            FA ESAN++K NILAQSGSYAM+QAN+ QQN+LRLL
Sbjct: 474  FAEESANFNKNNILAQSGSYAMSQANTVQQNILRLL 509
```

```
sp Q03843       Flagellin A [flaA] [Helicobacter pylori (Campylobacter      509
   FLAA_HELPY   pylori),                                                     AA
                Helicobacter pylori J99 (Campylobacter pylori J99)]          align


 Score =  438 bits (1126), Expect = e-121
 Identities = 261/576 (45%), Positives = 345/576 (59%), Gaps = 72/576 (12%)
```

```
Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
            F++NTN+ A+NA   S L   +L  SL RLSSGLRIN AADDASGM +ADSLRSQA++LG
Sbjct: 2   FQVNTNINAMNAHVQSALTQNALKTSLERLSSGLRINKAADDASGMTVADSLRSQASSLG 61

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QAI+N ND +GI+Q ADKAMDEQLKILDT+K KATQAAQDGQ+ ++R  +Q+DI +L++
Sbjct: 62  QAIANTNDGMGIIQVADKAMDEQLKILDTVKVKATQAAQDGQTTESRKAIQSDIVRLIQG 121

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
            LDNI NTT++NG+ LLSG FTN+EFQ+GA SNQ++KA+IG+T S KIG  R   TGA
Sbjct: 122 LDNIGNTTTYNGQALLSGQFTNKEFQVGAYSNQSIKASIGSTTSDKIGQVRIATGALITA 181

Query: 182 SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVY 241
            SG + LT K  +G+ D  ++V +S+S GTG+G LAE INK++++TGV+A   V TT
Sbjct: 182 SGDISLTFKQVDGVNDVTLESVKVSSSAGTGIGVLAEVINKNSNRTGVKAYASVITTSDV 241

Query: 242 AIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            A++ G+ S +  +NG+ +G I + K   D +G L++AINAV   TGV+A  D+  G
Sbjct: 242 AVQSGSLS-NLTLNGIHLGNIADIKKNDSDGRLVAAINAVTSETGVEAYTDQKG------ 294

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMIS-- 358
                                   RL+L  DGR I I  ++S  G    M++
Sbjct: 295 ------------------------RLNLRSIDGRGIEIKTDSVSN-GPSALTMVNGG 326

Query: 359 QSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXX 418
            Q      + G++S T DA            NV S S
Sbjct: 327 QDLTKGSTNYGRLSLTRLDAKSI-------------NVVSASDSQHLGFTAIGFGESQVA 373

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
               NL                  V+               A+     +G
Sbjct: 374 ETTVNLRDVTGNFNANVKSASGANYNAVI--------------------ASGNQSLGSG 412

Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
            VTTL+GAM V+DIAE+A+   LD++R+D+GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVD
Sbjct: 413 VTTLRGAMVVIDIAESAMKMLDKVRSDLGSVQNQMISTVNNISITQVNVKAAESQIRDVD 472

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLL 574
            FA ESAN++K NILAQSGSYAM+QAN+ QQN+LRLL
Sbjct: 473 FAEESANFNKNNILAQSGSYAMSQANTVQQNILRLL 508
```

tr Q8GD49 **Flagellin [flaB] [Helicobacter pylori (Campylobacter pylori)]** 514 AA

align

```
Score = 434 bits (1117), Expect = e-120
Identities = 275/587 (46%), Positives = 348/587 (58%), Gaps = 88/587 (14%)

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
            FRINTN+AAL + A    N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+  LG
Sbjct: 3   FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 62

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct: 63  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLEE 122
```

```
Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETG----- 176
           LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct: 123 LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE 182

Query: 177 -------AQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV 229
                  AQ+ T  VGL  K  NG+ D+K + V ISTS GTG+GAL+E IN+ ++  GV
Sbjct: 183 GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTSAGTGIGALSEIINRFSNTLGV 240

Query: 230 RATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQA 288
           RA+Y+V TG  ++ GT ++  INGV IG + +    D +G L +AIN+VK
Sbjct: 241 RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVK------- 292

Query: 289 SKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSA 348
                       D  G++ + DI             GR++L  DGR I++   + S
Sbjct: 293 ------------DRTGVEASLDI------------QGRINLHSIDGRAISVHAASASG 326

Query: 349 IGMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXX 408
             G +   S       G+++ T ADA         V  N S +
Sbjct: 327 QVFGGGNFAGISGTQ-HAVIGRLTLTRADARDI-------IVSGVNFSHVG-------- 369

Query: 409 XXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXQFAALKTT 468
                                       N    V                    A
Sbjct: 370 --------------------FHSAQGVAEYTVNLRAVRGIFDANVASAAGANANGAQA 407

Query: 469 AANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK 528
            N+    AGVT+LKGAM VMD+A++A T LD+IR+D+GS+Q ++ +TINNI+VTQVNVK
Sbjct: 408 ETNSQGIGAGVTSLKGAMIVMDMADSARTQLDKIRSDMGSVQMELVTTINNISVTQVNVK 467

Query: 529 AAESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           AAESQIRDVDFA ESAN+SK NILAQSGS+AMAQAN+ QQNVLRLLQ
Sbjct: 468 AAESQIRDVDFAEESANFSKYNILAQSGSFAMAQANAVQQNVLRLLQ 514
```

tr <u>Q6VYQ2</u> **Flagellin A [flaA] [Helicobacter pylori (Campylobacter**   510
            pylori)]   AA
                                                                            <u>align</u>

Score = 433 bits (1113), Expect = e-120
Identities = 259/576 (44%), Positives = 343/576 (58%), Gaps = 72/576 (12%)

```
Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
           F++NTN+ A+NA   S L  +L  SL RLSSGLRIN AADDASGM +ADSLRSQA++LG
Sbjct: 3   FQVNTNINAMNAHVQSALTQNALKTSLERLSSGLRINKAADDASGMTVADSLRSQASSLG 62

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
           QAI+N ND +GI+Q ADKAMDEQLKIL T+K KATQAAQDGQ+ ++R  +Q+DI +L++
Sbjct: 63  QAIANTNDGMGIIQVADKAMDEQLKILYTVKVKATQAAQDGQTTESRKAIQSDIVRLIQG 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
           LDNI NTT++NG+ LLSG FTN+EFQ+GA SNQ++KA+IG+T S KIG  R   TGA
Sbjct: 123 LDNIGNTTTYNGQALLSGQFTNKEFQVGAYSNQSIKASIGSTTSDKIGQVRIATGALITA 182

Query: 182 SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVY 241
           SG + LT K  +G+ D   ++V +S+S GTG+G LAE INK++++TGV+A   V TT
Sbjct: 183 SGDISLTFKQVDGVNDVTLESVKVSSSAGTGIGVLAEVINKNSNRTGVKAYASVITTSDV 242
```

```
Query: 242 AIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           A++ G+ S +  +NG+ +G I + K  D +G L++AINAV    TGV+A  D+ G
Sbjct: 243 AVQSGSLS-NLTLNGIHLGNIADIKKNDSDGRLVAAINAVTSETGVEAYTDQKG------ 295


Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINSGTNLSAIGMGTTDMIS-- 358
                                        RL+L  DGR I I  ++S  G     M++
Sbjct: 296 -------------------------RLNLRSIDGRGIEIKTDSVSN-GPSALTMVNGG 327


Query: 359 QSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXX 418
           Q      + G++S T  DA              NV S S
Sbjct: 328 QDLTKGSTNYGRLSLTRLDAKSI-------------NVVSASDSQHLGFTAIGFGESQVA 374


Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
              NL                      V+                   A+        +G
Sbjct: 375 ETTVNLRDVTGNFNANVKSASGANYNAVI--------------------ASGNQSLGSG 413


Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
           VTTL+GAM V+DIAE+A+   LD++R+D+GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVD
Sbjct: 414 VTTLRGAMVVIDIAESAMKMLDKVRSDLGSVQNQMISTVNNISITQVNVKAAESQIRDVD 473


Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLL 574
           FA ESAN++K NIL QSGSYAM+QAN+ QQN+LRLL
Sbjct: 474 FAEESANFNKNNILGQSGSYAMSQANTVQQNILRLL 509
```

```
tr    Q84IC0        Flagellin (Fragment) [flaA] [Campylobacter lari]  487 AA
                                                                        align


  Score =  412 bits (1059), Expect = e-114
  Identities = 214/305 (70%), Positives = 255/305 (83%), Gaps = 1/305 (0%)


Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1    GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60


Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
            GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61   GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120


Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
            ELDNIANTT++NGKQLLSG F+NQ+FQIG  +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121  ELDNIANTTTYNGKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT 180


Query: 181  TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240
             SG  G TIKNY+G+ DFK  +V++STS GTGLGALA EINKS+DKTGVRAT  V+T
Sbjct: 181  GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAAEINKSSDKTGVRATATVQTISS 240


Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
              I+ G T   F INGV IGK+  + GD +GSL++AINA KDTTGV+AS    NG+LVL S
Sbjct: 241  GTIQAGNTGDTFTINGVVIGKVAVQAGDKDGSLVAAINAKKDTTGVEASV-VNGQLVLNS 299


Query: 301  ADGRG 305
            ADGRG
Sbjct: 300  ADGRG 304
```

```
Score =  168 bits (426), Expect = 2e-40
Identities = 87/101 (86%), Positives = 97/101 (95%)

Query: 475  ETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQI 534
            ++AGVTTL+GAMAVMDIA+TAI NLD IRA+IG+ QNQ+TSTINNI+VTQVNVKAAESQI
Sbjct: 387  QSAGVTTLQGAMAVMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQI 446


Query: 535  RDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
            RDVDFASESANYSKANILAQSGSYAMAQAN++ QNVLRLLQ
Sbjct: 447  RDVDFASESANYSKANILAQSGSYAMAQANAASQNVLRLLQ 487
```

```
tr  Q8VN90  Flagellin A (Fragment) [flaA] [Helicobacter pylori        458
            (Campylobacter                                               AA
            pylori)]                                                     align
```

```
Score =  383 bits (983), Expect = e-105
Identities = 233/531 (43%), Positives = 309/531 (57%), Gaps = 80/531 (15%)

Query: 34   GLRINSAADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKT 93
            GLRIN AADDASGM +ADSLRSQA++LGQAI+N ND +GI+Q ADKAMDEQLKILDT+K
Sbjct: 1    GLRINKAADDASGMTVADSLRSQASSLGQAIANTNDGMGIIQVADKAMDEQLKILDTVKV 60


Query: 94   KATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSN 153
            KATQAAQDGQ+ ++R +Q+DI +L++ LDNI NTT++NG+ LLSG FTN+EFQ+GA SN
Sbjct: 61   KATQAAQDGQTTESRKAIQSDIVRLIQGLDNIGNTTTYNGQALLSGQFTNKEFQVGAYSN 120


Query: 154  QTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGL 213
            Q++KA+IG+T S KIG R  TGA  SG + LT K  +G+ D  ++V +S+S GTG+
Sbjct: 121  QSIKASIGSTTSDKIGQVRIATGALITASGDISLTFKQVDGVNDVTLESVKVSSSAGTGI 180


Query: 214  GALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGS 272
            G LAE INK+++++TGV+A  V TT   A++ G+ S +  +NG+ +G I + K  D +G
Sbjct: 181  GVLAEVINKNSNRTGVKAYASVITTSDVAVQSGSLS-NLTLNGIHLGNIADIKKNDSDGR 239


Query: 273  LISAINAVKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLV 332
            L++AINAV  TGV+A D+ G                              RL+L
Sbjct: 240  LVAAINAVTSETGVEAYTDQKG--------------------------------RLNLR 266


Query: 333  KNDGRDINI------SGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKG 386
            DGR I I    +G N  +  G D+  S+     + G++S T  DA
Sbjct: 267  SLDGRGIEIKTDSVSNGPNALTMVNGGQDLTKGST-----NYGRLSLTRLDAKSI----- 316


Query: 387  GGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXNTYV 446
                   NV S S                        NL                       V
Sbjct: 317  --------NVVSASDSQHLGFTAIGFGESQVAETTVNLRDVTGNFNANVKSASGANYNAV 368


Query: 447  VXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADI 506
            +                            A+       +GVTTL+GAM V+DIAE+A+  LD++R+D+
Sbjct: 369  I--------------------ASGNQSLGSGVTTLRGAMVVIDIAESAMKMLDKVRSDL 407


Query: 507  GSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGS 557
            GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVDFA ESAN++K NILAQSGS
Sbjct: 408  GSVQNQMISTVNNISITQVNVKAAESQIRDVDFAEESANFNKNNILAQSGS 458
```

```
tr  Q8VN91  Flagellin A (Fragment) [flaA] [Helicobacter pylori          458
             (Campylobacter                                              AA
             pylori)]                                                    align

 Score =  382 bits (982), Expect = e-105
 Identities = 232/527 (44%), Positives = 308/527 (58%), Gaps = 72/527 (13%)

Query:  34  GLRINSAADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKT 93
            GLRIN AADDASGM +ADSLRSQA++LGQAI+N ND +GI+Q ADKAMDEQLKILDT+K
Sbjct:   1  GLRINKAADDASGMTVADSLRSQASSLGQAIANTNDGMGIIQVADKAMDEQLKILDTVKV 60

Query:  94  KATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSN 153
            KATQAAQDGQ+ ++R  +Q+DI +L++ LDNI NTT++NG+ LLSG FTN+EFQ+GA SN
Sbjct:  61  KATQAAQDGQTTESRKAIQSDIVRLIQGLDNIGNTTTYNGQALLSGQFTNKEFQVGAYSN 120

Query: 154  QTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGL 213
            Q++KA+IG+T S KIG R  TGA   SG + LT K +G+ D   ++V +S+S GTG+
Sbjct: 121  QSIKASIGSTTSDKIGQVRIATGALITASGDISLTFKQVDGVNDVTLESVKVSSSAGTGI 180

Query: 214  GALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGS 272
            G LAE INK++++TGV+A   V TT   A++ G+ S +  +NG+ +G I + K  D +G
Sbjct: 181  GVLAEVINKNSNRTGVKAYASVITTSDVAVQSGSLS-NLTLNGIHLGNIADIKKNDSDGR 239

Query: 273  LISAINAVKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLV 332
            L++AINAV   TGV+A  D+ G                                RL+L
Sbjct: 240  LVAAINAVTSETGVEAYTDQKG--------------------------------RLNLR 266

Query: 333  KNDGRDINISGTNLSAIGMGTTDMIS--QSSVSLRESKGQISATNADAMGFNSYKGGGKF 390
              DGR I I  ++S G   M++ Q       + G++S T  DA
Sbjct: 267  SLDGRGIEIKTDSVSN-GPSALTMVNGGQDLTKGSTNYGRLSLTRLDAKSI--------- 316

Query: 391  VFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXX 450
                 NV S S                      NL                    V+
Sbjct: 317  ----NVVSASDSQHLGFTAIGFGESQVAETTVNLRDVTGNFNANVKSASGANYNAVI--- 369

Query: 451  XXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQ 510
                       A+       +GVTTL+GAM V+DIAE+A+  LD++R+D+GS+Q
Sbjct: 370  ------------------ASGNQSLGSGVTTLRGAMVVIDIAESAMKMLDKVRSDLGSVQ 411

Query: 511  NQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGS 557
            NQ+ ST+NNI++TQVNVKAAESQIRDVDFA ESAN++K NILAQSGS
Sbjct: 412  NQMISTVNNISITQVNVKAAESQIRDVDFAEESANFNKNNILAQSGS 458
```

```
tr  Q8VLN3  Flagellin A (Fragment) [flaA] [Helicobacter pylori          458
             (Campylobacter                                              AA
             pylori)]                                                    align

 Score =  382 bits (982), Expect = e-105
 Identities = 232/527 (44%), Positives = 308/527 (58%), Gaps = 72/527 (13%)

Query:  34  GLRINSAADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKT 93
            GLRIN AADDASGM +ADSLRSQA++LGQAI+N ND +GI+Q ADKAMDEQLKILDT+K
Sbjct:   1  GLRINKAADDASGMTVADSLRSQASSLGQAIANTNDGMGIIQVADKAMDEQLKILDTVKV 60

Query:  94  KATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSN 153
            KATQAAQDGQ+ ++R  +Q+DI +L++ LDNI NTT++NG+ LLSG FTN+EFQ+GA SN
```

```
Sbjct:  61  KATQAAQDGQTTESRKAIQSDIVRLIQGLDNIGNTTTYNGQALLSGQFTNKEFQVGAYSN  120

Query: 154  QTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGL  213
            Q++KA+IG+T S KIG  R  TGA     SG + LT K  +G+ D   ++V +S+S GTG+
Sbjct: 121  QSIKASIGSTTSDKIGQVRIATGALITASGDISLTFKQVDGVNDVTLESVKVSSSAGTGI  180

Query: 214  GALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGS  272
            G LAE INK++++TGV+A   V TT   A++ G+ S +  +NG+ +G I + K   D +G
Sbjct: 181  GVLAEVINKNSNRTGVKAYASVITTSDVAVQSGSLS-NLTLNGIHLGNIADIKKNDSDGR  239

Query: 273  LISAINAVKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLV  332
            L++AINAV   TGV+A   D+  G                                 RL+L
Sbjct: 240  LVAAINAVTSETGVEAYTDQKG--------------------------------RLNLR  266

Query: 333  KNDGRDINISGTNLSAIGMGTTDMIS--QSSVSLRESKGQISATNADAMGFNSYKGGGKF  390
                DGR I I  ++S G    M++  Q      + G++S T  DA
Sbjct: 267  SIDGRGIEIKTDSVSN-GPSALTMVNGGQDLTKGSTNYGRLSLTRLDAKSI--------  316

Query: 391  VFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXNTYVVXXX  450
                NV S S                      NL                      V+
Sbjct: 317  ----NVVSASDSQHLGFTAIGFGESQVAETTVNLRDVTGNFNANVKSASGANYNAVI---  369

Query: 451  XXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQ  510
                      A+        +GVTTL+GAM V+DIAE+A+   LD++R+D+GS+Q
Sbjct: 370  ----------------ASGNQSLGSGVTTLRGAMVVIDIAESAMKMLDKVRSDLGSVQ  411

Query: 511  NQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGS  557
            NQ+ ST+NNI++TQVNVKAAESQIRDVDFA ESAN++K NILAQSGS
Sbjct: 412  NQMISTVNNISITQVNVKAAESQIRDVDFAEESANFNKNNILAQSGS  458
```

sp <u>Q07910</u>   **Flagellin B (Flagellin N) [flaB] [Helicobacter mustelae]** 513 AA
    FLAB_HELMU

                                                                   <u>align</u>

 Score = 381 bits (978), Expect = e-104
 Identities = 216/405 (53%), Positives = 275/405 (67%), Gaps = 24/405 (5%)

```
Query:   2  FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG  61
            FRINTN+AALNA +        +++  SL +LSSGLRIN AADDASGMAIADSLRSQ+ +LG
Sbjct:   2  FRINTNIAALNAHSIGVQTNRNIAGSLEKLSSGLRINKAADDASGMAIADSLRSQSESLG  61

Query:  62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE  121
            QA+ N NDA+G++Q ADKAMDEQLKILDTIK KA QAAQDGQS ++R  LQ+DI +LMEE
Sbjct:  62  QAVRNANDAIGMIQIADKAMDEQLKILDTIKAKAIQAAQDGQSQESRRSLQSDIRRLMEE  121

Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET------  175
            LDNIANTTSFNG+Q+LSG FTN+EFQIGA SN TVKA+IG T S KIG  R ET
Sbjct: 122  LDNIANTTSFNGQQMLSGAFTNKEFQIGAYSNTTVKASIGPTSSDKIGHIRMETASFSGV  181

Query: 176  ------GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV  229
                  G   + T  V L  K  +G+  F+ +NV ISTS GTG+GAL+E IN+ +DK G+
Sbjct: 182  GMLASAGGNNLTE--VALNFKATDGVNSFELENVRISTSAGTGIGALSEVINRFSDKLGI  239

Query: 230  RATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQA  288
            RATY+V TG  +  GT +    INGV IG + E + D +G LI+AIN+VK+ TGV+A
```

```
Sbjct: 240 RATYNVMATGTSPVMSGTV-RGLVINGVRIGTVNEVRKNDSDGRLINAINSVKNQTGVEA 298

Query: 289 SKDENGKLVLTSADGRGIKITGD------IGVG--SGILANQKENYGRLSLVKNDGRDIN 340
            S D G++ L S DGR I + D      G G +GI N    GRL+L++ D RDI
Sbjct: 299 SLDITGRINLVSLDGRAISVHADGEASHVFGEGNFTGISGNNHAIVGRLTLIRTDARDII 358

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNSYK 385
            +SG N S IG+ +  +++++ +LR+ +G   A  A G N+ K
Sbjct: 359 VSGVNFSHIGLHSAQGVAETTANLRQLRGMFGADIASAAGANANK 403
```

tr Q7X2D0 **Flagellin B [flaB] [Helicobacter pylori (Campylobacter**   514
            pylori)]   AA
                                                                                 align

```
 Score = 380 bits (976), Expect = e-104
 Identities = 216/403 (53%), Positives = 278/403 (68%), Gaps = 24/403 (5%)

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
            FRINTN+AAL + A   N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+  LG
Sbjct: 3   FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 62

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct: 63  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRKALQSDIQRLLEE 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET------ 175
            LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct: 123 LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSAE 182

Query: 176 ------GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV 229
                  AQ+ T   VGL  K  NG+ D+K + V ISTS GTG+GAL+E IN+ ++   GV
Sbjct: 183 GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTSAGTGIGALSEIINRFSNTLGV 240

Query: 230 RATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQA 288
            RA+Y+V  TG   ++ GT +D  INGV IG + +    D +G LI+AIN+VKD TGV+A
Sbjct: 241 RASYNVMATGGTPVQSGTV-KDLTINGVEIGTVNDVHKNDADGRLINAINSVKDRTGVEA 299

Query: 289 SKDENGKLVLTSADGRGIKI-----TGDI---GVGSGILANQKENYGRLSLVKNDGRDIN 340
            S D G++ L S DGR I +     +G +   G +GI Q    GRL+L + D RDI
Sbjct: 300 SLDIQGRINLHSIDGRAISVHATSASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII 359

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS 383
            +SG N S +G +  +++ +V+LR  +G   A  A G N+
Sbjct: 360 VSGVNFSHVGFHSAQGVAEYTVNLRAVRGIFDANVASAAGANA 402
```

tr Q8RNU8 **Flagellin B subunit [flaB] [Helicobacter pylori (Campylobacter** 514 AA
            pylori)]
                                                                                align

```
 Score = 378 bits (970), Expect = e-103
 Identities = 214/403 (53%), Positives = 278/403 (68%), Gaps = 24/403 (5%)

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
```

```
                   FRINTN+AAL + A    N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+   LG
Sbjct: 3   FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 62

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
                   QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct: 63  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLEE 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET------ 175
                   LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct: 123 LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE 182

Query: 176 ------GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV 229
                       AQ+ T  VGL  K  NG+ D+K + V ISTS GTG+GAL+E IN+ ++  GV
Sbjct: 183 GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTSAGTGIGALSEIINRFSNTLGV 240

Query: 230 RATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQA 288
                   RA+Y+V  TG   ++ GT  ++  INGV IG + + +   D +G L +AIN+VKD TGV+A
Sbjct: 241 RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVRKNDADGRLTNAINSVKDRTGVEA 299

Query: 289 SKDENGKLVLTSADGRGIKI-----TGDI---GVGSGILANQKENYGRLSLVKNDGRDIN 340
                   S D  G++ L S DGR I +     +G +   G +GI  Q   GRL+L + D RDI
Sbjct: 300 SLDIQGRINLHSIDGRAISVHAASASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII 359

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS 383
                   +SG N S +G +   +++ +V+LR  +G   A  A G N+
Sbjct: 360 VSGVNFSHVGFHSAQGVAEYTVNLRAVRGIFDANVASAAGANA 402
```

sp Q07911   **Flagellin B (Flagellin N) [flaB] [Helicobacter pylori** 513 AA
  FLAB_HELPY **(Campylobacter pylori)]**
                                                                      align

```
 Score = 377 bits (967), Expect = e-103
 Identities = 214/403 (53%), Positives = 277/403 (68%), Gaps = 24/403 (5%)

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
                   FRINTN+AAL + A    N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+   LG
Sbjct: 2   FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 61

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
                   QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct: 62  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLEE 121

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET------ 175
                   LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct: 122 LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNATVKASIGSTSSDKIGHVRMETSSFSGA 181

Query: 176 ------GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV 229
                       AQ+ T  VGL  K  NG+ D+K + V ISTS GTG+GAL+E IN+ ++  GV
Sbjct: 182 GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTSAGTGIGALSEIINRFSNTLGV 239

Query: 230 RATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQA 288
                   RA+Y+V  TG   ++ GT  ++  INGV IG + +    D +G L +AIN+VKD TGV+A
Sbjct: 240 RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVKDRTGVEA 298

Query: 289 SKDENGKLVLTSADGRGIKI-----TGDI---GVGSGILANQKENYGRLSLVKNDGRDIN 340
```

```
                  S D  G++ L S DGR I +      +G +   G  +GI  Q   GRL+L + D RDI
Sbjct:  299  SLDIQGRINLHSIDGRAISVHAASASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII  358

Query:  341  ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS  383
                  +SG N S +G +   +++ +V+LR  +G  A  A A G N+
Sbjct:  359  VSGVNFSHVGFHSAQGVAEYTVNLRAVRGIFDANVASAAGANA  401
```

sp Q9ZMV8   **Flagellin B (Flagellin N) [flaB] [Helicobacter pylori J99** 513 AA
    FLAB_HELPJ   **(Campylobacter pylori J99)]**
                                                                           align

 Score = 377 bits (967), Expect = e-103
 Identities = 214/403 (53%), Positives = 277/403 (68%), Gaps = 24/403 (5%)

```
Query:    2  FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG  61
                  FRINTN+AAL + A    N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+  LG
Sbjct:    2  FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG  61

Query:   62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE  121
                  QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct:   62  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLEE  121

Query:  122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET------  175
                  LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct:  122  LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE  181

Query:  176  ------GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV  229
                       AQ+ T   VGL  K  NG+ D+K + V ISTS GTG+GAL+E IN+ ++   GV
Sbjct:  182  GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTSAGTGIGALSEIINRFSNTLGV  239

Query:  230  RATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQA  288
                  RA+Y+V  TG  ++ GT  ++  INGV IG + +   D +G L +AIN+VKD TGV+A
Sbjct:  240  RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVKDRTGVEA  298

Query:  289  SKDENGKLVLTSADGRGIKI-----TGDI---GVGSGILANQKENYGRLSLVKNDGRDIN  340
                  S D  G++ L S DGR I +      +G +   G  +GI  Q   GRL+L + D RDI
Sbjct:  299  SLDIQGRINLHSIDGRAISVHAASASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII  358

Query:  341  ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS  383
                  +SG N S +G +   +++ +V+LR  +G  A  A A G N+
Sbjct:  359  VSGVNFSHVGFHSAQGVAEYTVNLRAVRGIFDANVASAAGANA  401
```

tr Q6VYQ1 **Flagellin B [flaB] [Helicobacter pylori (Campylobacter**   514
          pylori)]   AA
                                                                           align

 Score = 377 bits (967), Expect = e-103
 Identities = 214/403 (53%), Positives = 277/403 (68%), Gaps = 24/403 (5%)

```
Query:    2  FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG  61
                  FRINTN+AAL + A    N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+  LG
Sbjct:    3  FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG  62
```

```
Query: 62   QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct: 63   QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLEE 122


Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET------ 175
            LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct: 123  LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE 182


Query: 176  ------GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV 229
                  AQ+ T VGL K NG+ D+K + V ISTS GTG+GAL+E IN+ ++  GV
Sbjct: 183  GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTSAGTGIGALSEIINRFSNTLGV 240


Query: 230  RATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQA 288
            RA+Y+V  TG  ++ GT  ++  INGV IG + +    D +G L +AIN+VKD TGV+A
Sbjct: 241  RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVKDRTGVEA 299


Query: 289  SKDENGKLVLTSADGRGIKI-----TGDI---GVGSGILANQKENYGRLSLVKNDGRDIN 340
            S D G++ L S DGR I +      +G +   G +GI Q   GRL+L + D RDI
Sbjct: 300  SLDIQGRINLHSIDGRAISVHAASASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII 359


Query: 341  ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS 383
            +SG N S +G +  +++ +V+LR  +G  A  A G N+
Sbjct: 360  VSGVNFSHVGFHSAQGVAEYTVNLRAVRGIFDANVASAAGANA 402
```


tr   Q9XB37   **Flagellin B [flaB] [Helicobacter felis]**   514 AA
                                                                  align


```
 Score =  373 bits (958), Expect = e-102
 Identities = 250/576 (43%), Positives = 322/576 (55%), Gaps = 66/576 (11%)

Query: 2    FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
            FRINTNVAALNA       N + L  SL +LSSGLRIN AADDASGMAIADSLRSQ+ +LG
Sbjct: 3    FRINTNVAALNAHTIGVRNNRDLSTSLEKLSSGLRINKAADDASGMAIADSLRSQSASLG 62


Query: 62   QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QA+ N NDA+G++QTADKAMDEQ+KILDT+KTKA QAAQDGQ+ +TR  LQ+DI +L+EE
Sbjct: 63   QAVRNANDAIGVVQTADKAMDEQIKILDTVKTKAVQAAQDGQTAETRKALQSDILRLLEE 122


Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
            LDNIANTTSFNG+QLL+G+F+N+EFQIGA SN T+KA+IG T S KIG  RFET A
Sbjct: 123  LDNIANTTSFNGQQLLAGSFSNKEFQIGAYSNTTIKASIGPTGSDKIGHVRFETSAM--- 179


Query: 182  SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVY 241
               + G+E           V G   L E
Sbjct: 180  ---------DRGGME------------VSAGAQNLKEV--------------------TL 198


Query: 242  AIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDE--NGKLVLT 299
             K+    DF + V  KI   G G G+L++  IN    T GV+A+      G+  +
Sbjct: 199  NFKQADAVNDFKLESV---KISTSAGTGLGALVNVINKNSSTLGVRATAVVLGTGENSVE 255


Query: 300  SADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQ 359
            S   G+ I G + +G+    +      GRL+  N ++    T + A    TD+  Q
Sbjct: 256  SGTINGLTINGVL-IGNVNDVQHNDRDGRLTNAINSVKE----RTGVEAY----TDI--Q 304


Query: 360  SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXX 419
```

```
                   ++LR + G+  +  +AD      + +  GG       + N  +I   +
Sbjct: 305 GRINLRSTDGRAISVHADGKTGHVFGGGNFRGISGNAHAIVGRLTLTKENARDIIVS--- 361

Query: 420 XXKNLXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGV 479
                   +                    N  +          A   A N     AGV
Sbjct: 362 ---GVNFSHVGLHSAQGVAEYTVNLQAIRGVFDANAASAGGGNANAAQAAFNFKGIGAGV 418

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
                   T+L+GAM VMD+AE+A   LD+IR+D+GS+Q ++ +TINNI+VTQVNVKAAESQIRDVDF
Sbjct: 419 TSLRGAMMVMDMAESARIQLDKIRSDLGSVQMELVTTINNISVTQVNVKAAESQIRDVDF 478

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
                   A ESA++SK NILAQSGS+AMAQAN+ QQNVLRLLQ
Sbjct: 479 AEESASFSKFNILAQSGSFAMAQANAVQQNVLRLLQ 514
```

tr Q7TTM9 **Major flagellin subunit FlaA_1 (Major flagellin subunit**   508
                FlaA_2)   AA
                [flaA_1] [Helicobacter hepaticus ATCC 51449]   align

 Score = 368 bits (944), Expect = e-100
 Identities = 206/395 (52%), Positives = 264/395 (66%), Gaps = 15/395 (3%)

```
Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
           F++NTNV ALNA A S    +L  S+ +LSSGLRIN AADDASGMAIADSLRSQA+ LG
Sbjct: 3   FQVNTNVNALNAHAQSTFTQYNLKNSMEKLSSGLRINKAADDASGMAIADSLRSQASALG 62

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
           QAI N ND +GI+Q ADKAMDEQLKILDTIK+KA QAAQDGQS ++R+M+Q DI +L+E
Sbjct: 63  QAIRNTNDGMGIIQIADKAMDEQLKILDTIKSKAVQAAQDGQSTQSRSMIQMDIIRLIEG 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
           LD+I N T++NG  LLSG FTN+EFQ+GA SNQ++K +IG+T S KIG  R ETGA
Sbjct: 123 LDSIGNNTTYNGMALLSGAFTNKEFQVGAYSNQSIKTSIGSTTSDKIGQVRIETGALVTA 182

Query: 182 SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVY 241
           SG V +T KN +G+ D  ++V +S S GTGLG LAE INK++DKTGVRA  +   TT
Sbjct: 183 SGEVTVTFKNVDGVNDITLESVKVSHSAGTGLGVLAEVINKNSDKTGVRAQANAYTTSDE 242

Query: 242 AIKEGTTSQDFAINGVTIGK-IEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           +IK G+ + +  +NGV+IG  I + D +G L+ A NA    TGV+A D  G+L+L S
Sbjct: 243 SIKSGSLA-NLMVNGVSIGDIIGIQKNDSDGRLVQAFNAATMHTGVEAYTDNLGRLMLRS 301

Query: 301 ADGRGIKITGDIGV-------------GSGILANQKENYGRLSLVKNDGRDINISGTNLS 347
            DGRGI + + V       G   L        NYGRLSLV+ D RDI +SG N+S
Sbjct: 302 TDGRGISLKANGAVPGQGNDVAITTVNGGHDLTTGANNYGRLSLVRTDARDIVVSGLNIS 361

Query: 348 AIGMGTTDMISQSSVSLRESKGQISATNADAMGFN 382
           + G        ++Q++ +LR+ KG +      A G N
Sbjct: 362 STGYNDDTKVAQTTTNLRDMKGVFNENVRSASGAN 396
```

tr Q7VF81 **Minor flagellin subunit FlaB [flaB] [Helicobacter hepaticus]** 514 AA

                                                                        align

```
sp    P50612        Flagellin A [flaA] [Helicobacter mustelae]  494 AA
      FLAA_HELMU                                                 align

 Score = 345 bits (886), Expect = 1e-93
 Identities = 204/406 (50%), Positives = 261/406 (64%), Gaps = 29/406 (7%)


Query: 2    FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
            F++NTN+ AL  A +      L  SL +LSSGLRIN AADDASGM I+DSLRSQA+ LG
Sbjct: 2    FQVNTNINALTTSAGA--TQLGLKNSLEKLSSGLRINKAADDASGMTISDSLRSQASALG 59

Query: 62   QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
            QAISN ND +GI+Q ADKAMDEQLKILDTIK KATQAAQDGQSL++R +Q+DI +L++
Sbjct: 60   QAISNANDGIGIIQVADKAMDEQLKILDTIKVKATQAAQDGQSLESRKAIQSDIIRLIQG 119

Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
            LDNI NTTS+NG+ LLSG +TN+EFQIG  SNQ++K ++G+T S KIG  R   TGA
Sbjct: 120  LDNIGNTTSYNGQSLLSGQWTNKEFQIGTYSNQSIKVSVGSTTSDKIGQVRINTGAMITA 179

Query: 182  SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVY 241
            +    LT K  NG    + V IS SVGTGLG LAE INK++DKTG+RA    V+TT
Sbjct: 180  ASEATLTFKQINGGGTSPLEGVKISHSVGTGLGVLAEVINKNSDKTGIRAKASVETTSDK 239

Query: 242  AIKEGTTSQDFAINGVTIGKI-EYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300
               I  G   ++  IN V IG I + K GD +G L+ AINA+  +TGV+AS D  G+L L S
Sbjct: 240  EIMSGNL-KNLTINDVNIGNIVDIKKGDADGRLVQAINALTSSTGVEASTDSKGRLNLRS 298

Query: 301  ADGRGIKITGD----------------IGVGSGILANQ-KENYGRLSLVKNDGRDINIS 342
            DGRGI + D                + G I   +    NYGRLSLV+ D RDI ++
Sbjct: 299  VDGRGIVLKADASEDNGDGKSAPMAIDAVNGGQSITDGEGAANYGRLSLVRLDARDIVLT 358

Query: 343  GTN------LSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFN 382
            ++          SAIG G  + ++ ++V+LR+  G+  A+   A G N
Sbjct: 359  SSDKPDENKFSAIGFGDNN-VAMATVNLRDVLGKFDASVKSASGAN 403
```


```
tr    Q93NM1     Flagellin A (Fragment) [flaA] [Campylobacter jejuni]  194 AA
                                                                        align

 Score = 337 bits (864), Expect = 4e-91
 Identities = 177/192 (92%), Positives = 185/192 (96%)

Query: 9    AALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 68
            AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN
Sbjct: 1    AALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 60

Query: 69   DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANT 128
            DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANT
Sbjct: 61   DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANT 120

Query: 129  TSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLT 188
            TSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +  +SG V  T
Sbjct: 121  TSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGERISSSGEVQFT 180

Query: 189  IKNYNGIEDFKF 200
            +KNYNGI+DFKF
```

Sbjct: 181 LKNYNGIDDFKF 192

tr Q93NM0   **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 194 AA
<u>align</u>

Score = 337 bits (864), Expect = 4e-91
Identities = 176/192 (91%), Positives = 185/192 (95%)

Query: 9   AALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 68
            AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN
Sbjct: 1   AALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 60

Query: 69   DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANT 128
            DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANT
Sbjct: 61   DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANT 120

Query: 129 TSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLT 188
            TSFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG + +SG V T
Sbjct: 121 TSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRISSSGEVQFT 180

Query: 189 IKNYNGIEDFKF 200
            +KNYNGI+DFKF
Sbjct: 181 LKNYNGIDDFKF 192

tr Q8VN93 **Flagellin B (Fragment) [flaB] [Helicobacter pylori**   461
          (Campylobacter   AA
          pylori)]   <u>align</u>

Score = 337 bits (863), Expect = 5e-91
Identities = 191/364 (52%), Positives = 249/364 (67%), Gaps = 24/364 (6%)

Query: 41   ADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQ 100
            ADD+SGMAIADSLRSQ+ LGQAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQ
Sbjct: 1   ADDSSGMAIADSLRSQSANLGQAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQ 60

Query: 101 DGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATI 160
            DGQ+L++R LQ+DI +L+EELDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+I
Sbjct: 61   DGQTLESRRALQSDIQRLLEELDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASI 120

Query: 161 GATQSSKIGVTRFET------------GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTS 208
            G+T S KIG R ET   AQ+ T VGL K NG+ D+K + V ISTS
Sbjct: 121 GSTSSDKIGHVRMETSSFSGEGMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTS 178

Query: 209 VGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDG 267
            GTG+GAL+E IN+ ++ GVRA+Y+V TG ++ GT ++ INGV IG + +
Sbjct: 179 AGTGIGALSEIINRFSNTLGVRASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKN 237

Query: 268 DGNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKI-----TGDI---GVGSGIL 319
            D +G L +AIN+VKD TGV+AS D G++ L S DGR I +   +G +   G +GI
Sbjct: 238 DADGRLTNAINSVKDRTGVEASMDIQGRINLHSIDGRAISVHAASASGQVFGGGNFAGIS 297

Query: 320 ANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAM 379
            Q   GRL+L + D RDI +SG N S +G +   +++ +V+LR +G A A A

```
Sbjct: 298 GTQHAVIGRLTLTRTDARDIIVSGVNFSHVGFHSAQGVAEYTVNLRAVRGIFDANVASAA 357

Query: 380 GFNS 383
            G N+
Sbjct: 358 GANA 361
```

```
Database: EXPASY/UniProt
    Posted date:  Aug 29, 2004 10:26 AM
  Number of letters in database: 494,584,931
  Number of sequences in database:  1,544,870
```

```
Lambda      K       H
   0.309    0.125    0.322
```

```
Gapped
Lambda      K       H
   0.267    0.0410    0.140
```

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
length of query: 575
length of database: 494,584,931
effective HSP length: 129
effective length of query: 446
effective length of database: 295,296,701
effective search space: 131702328646
effective search space used: 131702328646
T: 11
A: 40
X1: 16 ( 7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.7 bits)
S2: 76 (33.9 bits)
```

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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.24 sec, SCORE=26760, Nseq=2, Len=576

```
unk|VIRT9350|Blast_submission   -GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADS
tr|Q7X516                       MGFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADS
                                ******:.****:*** :*::.** ************************

unk|VIRT9350|Blast_submission   LGQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQ
tr|Q7X516                       LGQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQ
                                *****.*****:*****************************************

unk|VIRT9350|Blast_submission   EELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTR
tr|Q7X516                       EELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTR
                                ***************************************************

unk|VIRT9350|Blast_submission   FTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRAT
tr|Q7X516                       FTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRAT
                                ***************************************************

unk|VIRT9350|Blast_submission   VYAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDE
tr|Q7X516                       VYAIKEGTTSQDFAINGVAIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDE
                                ******************:**:*:*****.**.*:****************

unk|VIRT9350|Blast_submission   SADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMG
tr|Q7X516                       SADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMG
                                ***************************************************

unk|VIRT9350|Blast_submission   SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSR
tr|Q7X516                       SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSR
                                ***************************************************

unk|VIRT9350|Blast_submission   SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGSNSQFAALKTTAANT
tr|Q7X516                       SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGSNSQFAALKTTAANT
                                ***************************************************

unk|VIRT9350|Blast_submission   TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAES
tr|Q7X516                       TTLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAES
                                *****************************:***:  ****************

unk|VIRT9350|Blast_submission   ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
tr|Q7X516                       ASESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ
                                ******:** **********:***: *****:***
```